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<p>(54) Title: NOVEL INVERTASE GENE(S) AND USES THEREOF</p>			
<p>(57) Abstract</p> <p>Transgenic plants that are modified to produce fruits that have altered levels of soluble solids compared to non-transgenic plants of the same species are provided. The transgenic plants are prepared by introducing into plants DNA constructs that encode invertase operatively linked to DNA encoding regulatory regions that direct transcription of the DNA encoding invertase and operatively linked to DNA encoding amino acids that direct proper processing of the invertase through the secretory pathways of the plant and targeting of the invertase to the vacuole. In particular, DNA constructs encoding tomato plant vacuolar invertase in operative linkage with a developmentally regulated promoter region are provided. Preferred regulatory and structural DNA is obtained from genomic DNA clones and cDNA clones encoding tomato fruit vacuolar invertases from the commercial tomato plant, <i>Lycopersicon esculentum</i>, and wild tomato plant, <i>Lycopersicon pimpinellifolium</i>. Probes derived from the genomic DNA and cDNA, antibodies specific for tomato fruit invertase, and uses therefor, are also provided.</p>			

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-1-

NOVEL INVERTASE GENE(S) AND USES THEREOF

This application is a continuation-in-part of U.S. Patent Application Serial No. 07/771,331 to Fitzmaurice et al., filed October 4, 1991, "NOVEL INVERTASE GENE(S) AND USES THEREOF", which in turn is a continuation-in-part of U.S. Patent Application Serial No. 07/660,344 to Fitzmaurice et al., filed February 22, 1991, "NOVEL INVERTASE GENE(S) AND USES THEREOF". The subject matter of U.S. Patent Application Serial Nos. 07/771,331, and 07/660,344 are incorporated herein in their entirety by reference thereto.

FIELD OF THE INVENTION

The present invention is related to methods for improving the value of commercial varieties of plants by altering the phenotype of the plants and is related to the plants that exhibit the altered phenotype. In particular, this invention is related to transgenic tomato plants that have been genetically engineered to produce tomatoes that exhibit an altered solids content and an altered ratio of soluble solids to insoluble solids. Specifically, the solids content of the tomato fruit is altered by modifying the timing and level of expression of vacuolar invertase in ripening tomato fruit. This invention is also related to promoters and DNA for achieving such regulated expression in plants.

BACKGROUND OF THE INVENTION

Tomato solids include a water-soluble and a water-insoluble fraction. The insoluble solids in tomato fruit are primarily components of the cell wall and are responsible for the viscosity of processed tomato pulp. The water-soluble fraction contains the hexoses, glucose and fructose which constitute more than 90% of this fraction. Measurement of the content of these two sugars in a given fruit defines the "soluble solids content" of that fruit for commercial cultivars. The soluble solids content or ratio of soluble to insoluble solids is a major factor affecting the profitability of commercial

-2-

tomato processing operations. The solids content is also important in determining the flavor and marketability of fresh market tomatoes.

- The hexoses in ripened tomato fruit are produced by
- 5 hydrolysis of sucrose, which is transported from the leaves, and by hydrolysis of accumulated starch, which is also derived from sucrose transported into the fruit, during fruit development. The enzyme which catalyzes the conversion of sucrose to the hexoses glucose and
- 10 fructose, is beta-fructofuranosidase, commonly called invertase. Plants, including tomato, have at least two invertase activities, a soluble invertase located in the vacuole and an insoluble invertase activity bound to the cell wall.
- 15 There are characteristic differences in the activity of invertase and the distribution of sugars in plant tissues and in the fruit at different stages of ripeness. There are also differences in the activity profile of invertase and in the solids content among the fruits of
- 20 different tomato species. For example, invertase activity increases in tomato fruit during ripening. Also, the fruit of *Lycopersicon pimpinellifolium*, which is a wild tomato species, is richer in invertase and expresses it earlier during ripening, and exhibits a
- 25 higher soluble solids content than the cultivated tomato species, *Lycopersicon esculentum*.
- Tomato growers and processors strive to develop tomato fruit that reflects the specific balance of soluble solids content and insoluble solids content
- 30 desired for a particular tomato product. Traditionally, efforts to improve or alter this balance have focussed on the development of hybrid plants. For example, in an effort to increase the soluble solids content of cultivated tomatoes, such cultivated species have been
- 35 crossed with wild tomato species that produce fruit with

-3-

a higher soluble solids content than the cultivated varieties. The hybrid plants, however, not only acquire the desired trait but also tend to possess undesirable traits of the wild species.

5 There is a need, therefore, to produce improved versions of cultivated species of tomato, such as *L. esculentum*, that exhibit desirable traits of the wild species, such as a higher ratio of soluble solids to insoluble solids and a higher level of soluble solids, 10 but that do not also have the undesirable traits of the wild species.

It would also be desirable to have the ability to produce cultivated plants that produce fruit that have a selected specific level of soluble solids content and 15 ratio of soluble to insoluble solids content desired for a particular tomato product. In particular, it would be desirable to produce tomato fruit that have an increased soluble solids content as compared to that of presently available fruit and to thereby provide fruit that can be 20 processed more economically.

Therefore, it is an object of this invention to provide transgenic tomato plants that express invertase earlier during ripening and express higher levels of invertase during fruit ripening than cultivated non- 25 transgenic plants.

It is also an object of this invention to provide a means for regulating and altering the levels and ratios of soluble to insoluble solids in the fruit of cultivated tomato plants in order to select a specific level of 30 soluble solids content and ratio of soluble to insoluble solids content desired for a particular tomato product.

It is also an object of this invention to provide tomato fruits that exhibit such soluble solids content and ratio of soluble to insoluble solids content.

-4-

SUMMARY OF THE INVENTION

Transgenic tomato plants that have fruits with solids contents and ratios of soluble to insoluble solids that differ from non-transgenic plants of the same species are provided. In particular, transgenic tomato plants that produce fruits that have improved taste and processing properties are provided.

The altered soluble solids content and ratio of soluble to insoluble solids in tomato fruit are achieved by altering the timing of expression of an invertase and level of accumulation of such invertase in the vacuoles. The timing of expression of vacuolar invertase and the level of accumulation of vacuolar invertase in the plants are altered by increasing or decreasing expression of a gene or genes encoding invertase and by changing the time during the development of the plant, particularly the fruit, that one or more of such genes is expressed.

Methods for increasing the soluble solids content of tomato fruit produced by a tomato plant by introducing DNA constructs that contain DNA encoding an invertase are provided. The DNA construct encodes an invertase that is secreted and transported to the vacuoles or is modified so that the invertase is secreted and transported to the vacuoles.

In accordance with the methods, tomato plants are transformed with the constructs, and altered levels of invertase are expressed. In particular, DNA encoding the invertase is operatively linked to a promoter recognized by the plant RNA polymerase II. If the DNA encodes an invertase that is not a vacuolar invertase, DNA encoding the invertase is operatively linked to DNA that encodes vacuolar targeting sequences, and, if necessary, DNA encoding signal sequences.

Thus, a DNA construct encoding tomato fruit invertase under the control of a promoter that is

-5-

functional in plants is introduced into cells of a tomato plant, the cells containing the construct are cultured under conditions that result in the development of transgenic tomato plantlets, and the plantlets are grown 5 into tomato plants under conditions such that the DNA encoding tomato fruit invertase is expressed.

When recombinant tomato plants containing tomato fruit invertase under the transcriptional regulation of selected control sequences are grown, both the quantity 10 and the timing of tomato fruit invertase production can be altered. The manner in which invertase expression is altered is a function of the regulatory sequences to which the invertase-encoding DNA is operably linked. The resulting transgenic plants produce fruit that has a 15 soluble solids content and ratio of soluble solids to insoluble solids that differ from the non-transgenic plant.

DNA constructs made by fusing tomato invertase gene sequences with homologous or heterologous regulatory 20 sequences are also provided. In preferred embodiments, the regulatory sequences, particularly the promoter region, are selected such that the onset of expression of recombinant tomato fruit invertase commences at an earlier stage of development of the tomato fruit than 25 would otherwise occur when the same plant does not express the recombinant invertase. In particular, DNA encoding the invertase is operably linked to a developmentally regulated promoter selected so that the onset of expression of recombinant tomato fruit invertase 30 begins at about the breaker stage of development of tomato fruit and continues until the tomato fruit has reached the red stage. The tomato fruit of a transgenic plant that contains this DNA construct should have a 35 soluble solids content higher than the soluble solids content of tomato fruit produced by equivalent non-

-6-

recombinant tomato plants. It is preferred that the transgenic fruit have a soluble solids content at least about 0.5% higher, preferably about 1% or more, than fruit of non-modified tomato plants.

5 DNA constructs including regulatory regions which contain fruit-specific developmentally controlled regulatory regions are provided. These regulatory regions include promoter regions that are effective for achieving regulated expression of heterologous DNA in
10 transgenic plants.

The preferred promoter regions include, but are not limited to, constitutive promoters, such as the CaMV 35S promoter, and developmentally regulated promoters that confer fruit specificity and appropriate temporal control
15 on the expression of the DNA encoding invertase. Such promoters include native *Lycopersicon* invertase promoters: DNA encoding regulatory regions upstream from the translation start codon of the structural invertase genes in the genomic clones from *L. esculentum* and *L.*
20 *pimpinellifolium* and from other developmentally regulated genes are provided.

In addition, DNA encoding proteins and sequences that direct such proteins to the vacuoles are also provided. Such DNA encodes proteins that include signal
25 sequences and specific C-terminal precursor peptide sequences, which target or sort proteins to the vacuole. DNA encoding such targeting and signal sequences may be operatively linked to DNA encoding an invertase that lacks such sequences. In preferred embodiments, such
30 proteins include the tomato fruit invertase signal sequence, which includes amino acids 1-47 and 48-92 of Seq. ID No. 1, and an invertase carboxyl-terminal precursor or propeptide sequence, that includes residues 607-613 of Seq. ID No. 1, preferably included as part of
35 the last 39 amino acids of tomato invertase (amino acids

-7-

598-636 in Seq. ID No. 1) or a portion thereof that is sufficient to effect vacuolar targeting.

The constructs may be used to produce *L. esculentum* transgenic plants, or other transgenic plants, that 5 express heterologous genes in a developmentally regulated manner. In particular, these constructs may be used to produce *L. esculentum* transgenic plants, or other transgenic plants, that express invertase under the control of the regulatory regions such that the levels of 10 invertase expressed and the timing of expression of invertase differ from nontransgenic plants and the levels of soluble and insoluble solids in the transgenic tomato fruits differ from the fruits of nontransgenic plants.

In most preferred embodiments, DNA constructs 15 containing the DNA encoding invertase from *L. esculentum* or *L. pimpinellifolium* operatively linked to DNA encoding the regulatory region of the invertase gene from *L. pimpinellifolium* or from other developmentally regulated genes that are expressed early during fruit 20 ripening are introduced into a cultivated tomato species, such as *L. esculentum*, to produce transgenic plants that have an altered phenotype manifested as increased production of invertase earlier in fruit development as compared to that produced in the non-transgenic plants. 25 Such transgenic tomato plants also can be used as a source for the production of substantially pure tomato fruit invertase and for the production of seeds that contain the heterologous DNA. Transgenic tomato plants in which the DNA encoding a mature invertase is operably 30 linked to a secretion signal sequence, vacuolar targeting signals and to developmentally regulated promoter regions isolated from plants of the genus *Lycopersicon* are provided. Constructs including these signals and heterologous DNA for the purpose of producing transgenic 35 tomato plants are also provided.

-8-

In accordance with other embodiments, transgenic plants that express lower levels of soluble solids than the non-transgenic plant and methods for decreasing the soluble solids content of tomato fruit are provided.

- 5 Production of tomato fruits that have decreased soluble solids content is desirable when one seeks to obtain tomato fruit having a higher ratio of insoluble to soluble solids. Cultivars capable of producing fruit with a higher ratio of insoluble to soluble solids are of
10 commercial value for the production of tomato products with high viscosity, such as tomato paste.

Transgenic plants that produce fruits that contain DNA constructs that result in decreased expression of invertase are provided. Reduced expression may be
15 effected by methods such as cosuppression [for a discussion of cosuppression see Hooper, C. (1991) *J. NIH Res.* 3:49-54], by operatively linking a truncated form of a tomato fruit invertase gene to a promoter, or by expression of invertase antisense mRNA. Antisense RNA
20 forms double-stranded RNA with the mRNA produced from the endogenous gene, thereby interfering with translation of the endogenous mRNA [see, e.g., Lichtenstein (1988) *Nature* 333:801-802]. To inhibit expression of the targeted gene, the antisense RNA can be less than full-
25 length copy of the targeted mRNA [see, e.g., Grum et al. (1988) *Nuc. Acids Res.* 16: 4569-4581 and references cited therein].

In plants that express antisense invertase mRNA or truncated forms of the protein, the amount of invertase
30 produced in the plant, particularly during fruit development, is substantially less than the amount of invertase produced when the plant does not express antisense invertase mRNA or a truncated form of invertase. The resulting fruit should have reduced
35 levels of the hexoses. In preferred embodiments, such

-9-

reduced levels in tomato fruit can be achieved by expressing, starting at the breaker stage and continuing through the ripe stage of fruit development, an antisense copy of part, or all, of the tomato fruit invertase mRNA or a truncated form of invertase mRNA in tomato fruit. As a result, reduced amounts of invertase are produced, and sucrose, which ordinarily would have been converted to glucose and fructose, may be converted into cell wall components.

10 In accordance with yet another embodiment, a tomato fruit produced by a transgenic tomato plant of the genus *Lycopersicon*, which is derived from a transgenic tomato plantlet which contains a recombinant construct encoding antisense tomato fruit invertase mRNA, such that the 15 total soluble solids content and ratio of soluble to insoluble solids content of the fruit is altered by virtue of the decreased conversion of sucrose into the hexoses.

20 In accordance with a further embodiment, methods for identifying the presence of invertase-encoding nucleic acid sequences by contacting a sample containing RNA or single-stranded DNA with a probe containing all or at least a portion of the nucleic acid sequence set forth in Seq. ID Nos. 1, 2, or 4 are provided. Hybridizing DNA 25 that encodes all or a portion of an invertase is isolated. In instances in which such hybridizing DNA encodes a portion of the invertase, it may be used to isolate full-length clones.

In preferred embodiments, isolated, substantially 30 pure DNA encoding vacuolar invertases that have amino acid sequences substantially identical to the vacuolar invertases of the commercial tomato species, *L. esculentum*, and the wild tomato species *L. pimpinellifolium*, are provided. Genomic DNA and cDNA

-10-

clones that encode the vacuolar invertase from each species are also provided.

Protoplasts containing the DNA constructs and seeds produced by the transgenic plants that include DNA that 5 encodes the exogenous or heterologous invertase are also provided.

In accordance with still further embodiments, methods for determining the tomato fruit invertase content of a sample; methods for identifying the presence 10 of invertase-encoding sequences in a cDNA expression library; methods for the recombinant production of tomato fruit invertase; methods for modulating the expression of tomato fruit invertase in solanaceous plant species; and methods for targeting protein product(s) expressed from 15 heterologous genes by recombinant plants to the vacuoles are provided.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

Definitions

Unless defined otherwise, all technical and 20 scientific terms used herein have the same meaning as is commonly understood by one of skill in the art. All publications mentioned herein are incorporated by reference thereto. All U.S. patents and publications cited herein are incorporated in their entirety by 25 reference thereto.

As used herein, invertase refers to an enzyme that hydrolyzes sucrose to fructose and glucose and encompasses any protein that exhibits this activity in plants. The biological activity of invertase may be 30 measured by one of several bioassays well-known in the art in which the sugars liberated by invertase activity are chemically quantified. Preferred invertases are those that, upon expression in a tomato plant, are transported through the processing pathway of the plant

-11-

and targeted to the vacuoles. Tomato fruit vacuolar invertase is among those preferred herein.

As used herein, a precursor invertase refers to a protein that includes a leader or signal sequence that
5 effects transport of the protein through plant processing pathways to yield mature protein and that includes a vacuolar targeting sequence to direct or sort the invertase to the vacuole. In the plant, signal sequences promote uptake of the protein into the endoplasmic
10 reticulum (ER) of the plant cells.

As used herein, a signal or leader sequence, which expressions are used interchangeably, refers to a sequence of amino acids that directs transport of the translation product through the processing pathway of the
15 host and results in the generation of a mature protein. The signal sequence includes or is modified to include one or a sequence of amino acids that is recognized by one or more host cell proteases. Such sequences may be interposed between the signal sequence and the protein,
20 whereby, upon recognition of the processing site by the appropriate host cell protease, removal of the signal sequence may be effected. The signal sequence, processing sites and protein are referred to as a precursor protein, and the processed protein is referred
25 to as the mature protein.

As used herein, regulatory sequences or signals also include sequences that are required for targeting proteins to selected plant organs, such as the vacuoles. Such sequences, vacuolar targeting sequences, present on
30 the C-terminal end of the protein, effect transport of the protein to which they are linked to the vacuoles. If such sequence is absent and no other targeting sequence is present, the protein is directed to the default pathway and ultimately to the cell wall.

-12-

- The processing sequences, signal sequences and targeting sequences for use herein are those that are sufficient for directing mature invertase protein to which such sequences are linked to the vacuoles of the
- 5 plant host in which the invertase is expressed. Any peptide or DNA encoding such peptide that effects proper processing and vacuolar targeting in plant hosts is contemplated for use herein. The preferred processing, signal, and targeting sequences for use herein are those
- 10 that effect proper secretion, processing and targeting of the *L. esculentum* vacuolar invertase. These preferred signal sequences and targeting sequences include, but are not limited to, the vacuolar invertase signal sequence and carboxyl-terminal peptide. Other such sequences that
- 15 are active in plants, such as the carboxyl-terminal propeptide (CTPP) of the barley lectin proprotein, the β -1,3-glucanase CTPPs of *Nicotiana tabacum* and *N. plumbaginifolia*, may also be used. The seven amino acids near the C-terminus of tomato fruit vacuolar invertase
- 20 (amino acids 607 to 613 of Seq. ID No. 1) have 86% sequence similarity to a 7-residue region of the C-terminus of β -1,3-glucanase from *Nicotiana plumbaginifolia*, which is non-homologous to invertase in the rest of its sequence.
- 25 As used herein, precursor invertase refers to unprocessed invertase that includes sequences that direct the protein through the processing pathways of the plant. Such invertase includes the signal sequences and vacuolar targeting or sorting sequences.
- 30 As used herein, exogenous invertase refers to invertase that is encoded by DNA that is introduced into the plant and is expressed in the plant in addition to endogenous invertase. The exogenous invertase may be the same as the endogenous invertase. For example, in
- 35 certain embodiments, the level of invertase expressed in

-13-

the plant is altered by introducing a DNA construct that encodes a *Lycopersicon* invertase.

As used herein, heterologous or foreign DNA and RNA are used interchangeably and refer to DNA or RNA that 5 does not occur naturally as part of the genome in which it is present or which is found in a location or locations in the genome that differ from that in which it occurs in nature. Examples of heterologous DNA include, but are not limited to, DNA that encodes exogenous 10 invertase and DNA that encodes RNA or proteins that mediate or alter expression of endogenous DNA by affecting transcription, translation, or other regulatable biochemical processes.

As used herein, operative linkage of heterologous 15 DNA to regulatory and effector sequences of nucleotides, such as promoters, enhancers, transcriptional and translational stop sites, and other signal sequences, refers to the functional relationship between such DNA and such sequences of nucleotides. For example, 20 operative linkage of heterologous DNA to a promoter refers to the physical and functional relationship between the DNA and the promoter such that the transcription of such DNA is initiated from the promoter by an RNA polymerase that specifically recognizes, binds 25 to and transcribes the DNA in reading frame.

As used herein, isolated, substantially pure DNA refers to DNA fragments purified according to standard techniques employed by those skilled in the art, such as that found in Maniatis et al. [(1982) *Molecular Cloning: 30 A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY].

As used herein, expression refers to the process by which nucleic acid is transcribed into mRNA and translated into peptides, polypeptides, r proteins. If 35 the nucleic acid is derived from genomic DNA, expression

-14-

may, if an appropriate eukaryotic host cell or organism is selected, include splicing of the mRNA.

As used herein, vector or plasmid refers to discrete elements that are used to introduce heterologous DNA into 5 cells for either expression of the heterologous DNA or for replication of the cloned heterologous DNA.

Selection and use of such vectors and plasmids are well within the level of skill of the art.

As used herein, expression vector includes vectors 10 capable of expressing DNA fragments that are in operative linkage with regulatory sequences, such as promoter regions, that are capable of effecting expression of such DNA fragments. Thus, an expression vector refers to a recombinant DNA or RNA construct, such as a plasmid, a 15 phage, recombinant virus or other vector that, upon introduction into an appropriate host cell, results in expression of the cloned DNA. Appropriate expression vectors are well known to those of skill in the art and include those that are replicable in eukaryotic cells 20 and/or prokaryotic cells and those that remain episomal or may integrate into the host cell genome.

As used herein, a promoter region refers to the portion of DNA of a gene that controls transcription of DNA to which it is operatively linked. The promoter 25 region includes specific sequences of DNA that are sufficient for RNA polymerase recognition, binding and transcription initiation. This portion of the promoter region is referred to as the promoter. In addition, the promoter region includes sequences that modulate this 30 recognition, binding and transcription initiation activity of the RNA polymerase. These sequences may be *cis* acting or may be responsive to *trans* acting factors. Promoters, depending upon the nature of the regulation, may be constitutive or regulated. A developmentally

-15-

regulated promoter is one that is turned on or off as a function of development.

As used herein, expression cassette refers to a DNA construct that includes DNA sequences that are functional for expression or encodes RNA or peptides functional for expression, and, if desired, processing and secretion of a mature protein in a selected host. Since such fragments are designed to be moved from vector to vector and into the host cell for both replication and expression, they are often referred to by those of skill in the art as "expression cassettes" or "cassettes". Accordingly an expression cassette includes DNA encoding a promoter region, a transcription terminator region, and sequences sufficient for translation, as well as any other regulatory signals, such as those that effect proper processing of the expressed protein or peptide.

As used herein, the term DNA construct embraces expression cassettes and includes DNA fragments that include more than one expression cassette.

As used herein, portions or fragments of the DNA constructs and expression cassettes are said to be operationally associated or operably or operatively linked when protein-encoding portions and regulatory regions are positioned such that expression, including transcription, translation and processing, of the protein-encoding regions is regulated by the DNA that encodes the regulatory regions.

As used herein, reference to "downstream" and "upstream" refers to location with respect to the direction of transcription from the promoter which regulates transcription of the invertase-encoding fragment.

As used herein, transgenic plants refer to plants containing heterologous or foreign DNA or plants in which the expression of a gene naturally present in the plant

-16-

has been altered. Such DNA is said to be in operative linkage with plant biochemical regulatory signals and sequences. Expression may be constitutive or may be regulatable. The DNA may be integrated into a chromosome 5 or integrated into an episomal element, such as the chloroplast, or may remain as an episomal element. In addition, any method for introduction of such DNA known to those of skill in the art may be employed.

As used herein, wild type plant refers to plants 10 that are of the same species or are identical to the transgenic plants, but do not contain DNA or RNA that encodes the heterologous gene that may be expressed by the transgenic plant.

As used herein, homologous invertase refers to a 15 protein that is sufficiently similar to tomato vacuolar invertase to catalyze the hydrolysis of sucrose to glucose and fructose and to so in the tomato plant.

As used herein, substantially homologous DNA refers to DNA that includes a sequence of nucleotides that is 20 sufficiently similar to another such sequence to form stable hybrids under specified conditions. As used herein, substantially homologous DNA that encodes invertase includes DNA that hybridizes under conditions of low stringency to DNA that encodes an invertase and 25 that encodes an invertase that functions as defined herein.

As used herein, a nucleic acid probe is a DNA or RNA fragment that includes a sufficient number of nucleotides to specifically hybridize to DNA or RNA that includes 30 identical or closely related sequences of nucleotides. A probe may contain any number of nucleotides, from as few as about 10 and as many as hundreds of thousands of nucleotides. The conditions and protocols for such hybridization reactions are well known to those of skill 35 in the art as are the effects of probe size, temperature,

-17-

degree of mismatch, salt concentration and other parameters on the hybridization reaction. For example, two single-stranded nucleic acid segments have "substantially the same sequence," within the meaning of 5 the present specification, if (a) both form a base-paired duplex with the same segment, and (b) the melting temperatures of the two duplexes in a solution of 0.5 X SSPE differ by less than 10°C. If the segments being compared have the same number of bases, then to have 10 "substantially the same sequence", they will typically differ in their sequences at fewer than 1 base in 10.

As used herein, conditions under which DNA molecules form stable hybrids and are considered substantially homologous are such that the DNA molecules with at least 15 about 60% complementarity form stable hybrids. Such DNA fragments are herein considered to be "substantially homologous". In particular, DNA that encodes invertase is substantially homologous to another DNA fragment if the DNA forms stable hybrids such that the sequences of 20 the fragments are at least about 60% complementary and if a protein encoded by the DNA is invertase, i.e., catalyzes the conversion of sucrose into the hexoses, glucose and fructose. Thus, any nucleic acid molecule that hybridizes with nucleic acid that encodes all or 25 sufficient portion of invertase to be used as a probe, and that encodes invertase is contemplated for use in preparing DNA constructs and transgenic tomato plants as described herein.

As used herein, breaker stage refers to the stage in 30 fruit ripening at which the color of the fruit exhibits a definite break in color from green to tannish-yellow, pink or red, on not more than about 10% of the surface of the tomato fruit. When more than 10%, but less than about 35 30% of the fruit surface, in the aggregate, shows a definite change in color from green to tannish-yellow,

-18-

pink, red, or a combination thereof, the fruit is said to be at the "turning" stage. When more than 30%, but less than about 60% of the fruit surface, in the aggregate, is pink or red, the fruit is said to be at the "pink" stage,
5 which is also the 3-inch intermediate stage, of development.

As used herein, all assays and procedures, such as hybridization reactions and antibody-antigen reactions, unless otherwise specified, are conducted under
10 conditions recognized by those of skill in the art as standard conditions.

Preparation of transgenic tomato plants.

Transgenic tomato plants that express altered levels of invertase and produce fruits that exhibit altered
15 solids content compared to non-transgenic plants are provided. The transgenic plants contemplated herein include those in which a heterologous or foreign gene encoding invertase, encoding an antisense invertase mRNA or encoding a truncated form of invertase has been
20 inserted into the genome or into an episomal element. By virtue of the presence of the heterologous DNA, the plant is engineered to express a desired phenotype, including an altered soluble or insoluble solids content in the fruit, or to produce a protein, which can then be
25 isolated upon harvesting the plant.

The preferred transgenic plants provided herein are transgenic tomato plants that express DNA encoding invertase under the control of either a constitutive or a developmentally regulated promoter region that is
30 recognized by the tomato plant transcriptional machinery, including *trans* acting regulatory factors and RNA polymerase II, so that expression of the invertase is either constitutive or is developmentally regulated. In addition, the DNA introduced into the plant should
35 include sequences that insure that the invertase that is

-19-

expressed in the transgenic tomato plant is processed through the plant processing pathway that directs it to the vacuoles. Consequently, the DNA encoding the invertase must also encode the necessary regulatory sequences, including a signal sequence and vacuolar targeting sequence, to target the invertase to the vacuole. Such signals and targeting sequences may be isolated as part of the DNA encoding the invertase, if the invertase is a vacuolar invertase, or the DNA 5 encoding the regulatory sequences may be operatively linked to the DNA that encodes the invertase.

The transgenic plants that contain and express invertase that is targeted to the vacuoles can be propagated and grown to produce fruit that exhibit an 10 altered soluble solids content, altered insoluble solids content, or altered ratio of soluble to insoluble solids 15 compared to the soluble and insoluble solids content of tomato fruit produced by unmodified tomato plants.

Transgenic tomato plantlets (*L. esculentum* cv. UC82) 20 that contain DNA constructs encoding invertase in operative linkage with a promoter recognized by the plant RNA polymerase II have been regenerated in tissue culture. Such plantlets were produced by transformation of tomato with various DNA constructs prepared herein, 25 including constructs in which the *L. esculentum* histidine decarboxylase (HDC) promoter, the *L. esculentum* invertase promoter, the *L. pimpinellifolium* invertase promoter, or the CaMV 35S promoter is fused to DNA encoding the *L. esculentum* tomato fruit vacuolar 30 invertase.

The ratio of insoluble solids to soluble solids in tomato fruit may also be altered by operatively linking promoters to DNA encoding antisense or truncated forms of invertase. Expressing an antisense invertase mRNA or a 35 truncated inactive form of invertase should result in

-20-

reduced levels of the invertase gene product in the cell. Constructs that include truncated forms of invertase and that encode antisense invertase mRNA have been constructed. Such constructs have been introduced into 5 tomato plants. These transgenic plants will be assayed for reduced expression of endogenous invertase.

Preparation of DNA constructs that encode invertase.

The DNA constructs containing DNA encoding invertase 10 in operative linkage with regulatory sequences effective for expression and vacuolar targeting of the encoded invertase are prepared. These DNA constructs are alternatively referred to as recombinant DNA constructs, that is, fusions of various sequences, and may be 15 produced using recombinant techniques well known in the art. The DNA constructs contain regulatory regions including promoters, transcription initiation sites, transcription termination sites, and, if necessary, vacuole sorting sequences, including signal sequences and 20 carboxyl-terminal propeptides. Any or all of these component sequences may be homologous or heterologous to the host plant cell. Additional heterologous sequences may also be included if needed to facilitate transformation of the plant cell with the constructs or 25 expression and proper processing and transport of the invertase.

The DNA constructs contain invertase-encoding sequences of nucleotides operably linked to genomic regulatory regions, including promoter regions. If the 30 invertase encoded by the DNA is not directed to the vacuoles, DNA encoding appropriate regulatory sequences, such as the invertase signal and vacuolar targeting sequences, can be operably linked to the invertase coding DNA. Any sequence effective for such targeting may be 35 used, such as, for example, the DNA encoding at least residues 607-613 of Seq. ID No. 1 and preferably residues

-21-

598-636 of Seq. ID No. 1 or a portion thereof that includes residues 607-613 and is effective for vacuolar targeting or DNA encoding any sequence of amino acids known or shown to effect vacuolar targeting. Such sequences may be empirically identified or isolated from 5 DNA that encodes proteins known to be directed to the vacuoles.

Isolation of DNA encoding invertase.

DNA encoding an invertase may be identified using 10 the DNA or antiserum provided herein using any method known to those of skill in the art. DNA encoding any invertase that functions in a plant host, provided that it is operatively linked to sequences that effect vacuolar targeting, is contemplated for use herein.

15 DNA encoding invertase may be isolated by screening a library with all or a portion of DNA encoding tomato vacuolar invertase protein, which can be employed as a probe, for the identification and isolation of invertase-encoding sequences from an appropriate cDNA or genomic 20 library or other sample containing DNA and RNA from plant and animal species. In particular, all, or a portion sufficient to identify related DNA, of the DNA encoding invertase provided herein is used a probe to isolate related DNA fragments.

25 Standard hybridization or other isolation techniques, as well known by those of skill in the art, can readily be employed for such purposes. Probes employed for such purpose typically have at least 14 nucleotides. Preferred probes employed for such purpose 30 are those of at least about 50 nucleotides in length, and may include portions from the nucleotide sequence set forth in Seq. ID Nos. 1 or 4, or the various DNA molecules which encode the amino acid sequence set forth in Seq. ID No. 1; with nucleotide sequences of about 100 35 nucleotides or greater being specially preferred.

-22-

Examples of such especially preferred sequences are those that have sequences set forth in Seq. ID No. 1, particular from the 5' coding region and the sequences encoding and surrounding what appears to be the active site of invertase, amino acid residues 295-307, particularly residues 298-306, of Seq. I.D. No. 1.

An exemplary 5' probe would be derived from the sequence of nucleotides 316-416 as set forth in Seq. ID No. 1; while an exemplary "active site" probe would be derived from the sequence of nucleotides 880-980 as set forth in Seq. ID No. 1. For ease of detection, such probes can be labeled with radioactive, chemiluminescent, or the like, labels.

The selected hybridizing DNA fragments may be characterized in order to ascertain whether they encode a full-length protein. If they do not, they may be used as probes to isolate full-length clones. The full-length clones may then be used to express the encoded protein, which may be assayed using standard assays for invertase activity, as defined herein. Selected full-length clones that encode invertase are then assessed for the presence of DNA encoding appropriate signal and vacuolar targeting sequences by any method known to the art, including producing transgenic plants and assaying for cloned invertase in the vacuole. If such signals are absent, the selected full-length clones may be modified by operatively linking such signals.

In addition, DNA encoding invertase that is not substantially homologous to tomato fruit invertase, such as yeast invertase, may be modified by the methods herein to produce DNA encoding an invertase that is properly sorted and targeted to the vacuoles. Such modified DNA is suitable for use herein.

The cDNA provided herein has been used to obtain genomic clones and also to obtain DNA encoding invertase

-23-

from a related species. DNA encoding tomato fruit vacuolar invertase has been isolated by screening *L. esculentum* cDNA expression libraries with antisera raised against vacuolar invertase purified from *L. esculentum* fruit. The isolated cDNA was used to screen *L. esculentum* and *L. pimpinellifolium* genomic DNA libraries for invertase gene promoter sequences and *L. pimpinellifolium* cDNA libraries for DNA sequences encoding *L. pimpinellifolium* vacuolar invertase. In like manner the DNA and/or antiserum provided herein may be employed to isolate DNA encoding invertases from other sources.

DNA encoding tomato fruit vacuolar invertase has also been isolated herein using polyclonal antibodies that specifically bind to purified tomato fruit vacuolar invertase. These antibodies are specifically reactive with peptide sequences of tomato fruit invertase, but are substantially unreactive with other glycoproteins or glycan-containing groups. In addition, these antibodies can be employed in a variety of methods, including methods for determining the tomato fruit invertase content of a sample. Those of skill in the art can readily determine methodologies for using antibodies to measure the tomato fruit invertase content of a sample. See, for example, Clausen (1981) *Immunochemical Techniques for the Identification and Estimation of Macromolecules*, 2nd ed., Elsevier/North-Holland Biomedical Press, Amsterdam, the Netherlands.

The DNA encoding an invertase may also be isolated by screening a cDNA library with such antibodies in order to detect translation products of cDNA clones that encode all or a part of a vacuolar invertase or by screening a cDNA or genomic library with the DNA provided herein that encodes invertase. Use of these antibodies and DNA to identify cDNAs may be accomplished using methods known to

-24-

those of skill in the art [see e.g., Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual*, Vol. 2, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp. 12.1-12.44; Morton et al. (1987) *J. Biol. Chem.* 5 262: 11904-11907]. The antibodies have been used to screen a cDNA expression library and to identify DNA encoding tomato fruit vacuolar invertase. Expression libraries were prepared from poly(A)+ RNA isolated from the "pink" stage fruit of each tomato species. The 10 libraries were screened with the antibodies made against purified tomato fruit vacuolar invertase.

Selected clones, obtained using any screening method, may, if necessary, be used to obtain full-length clones. The clones may then be tested by any manner 15 known to those of skill in the art in order to ascertain whether the DNA encoding invertase includes sequences sufficient to direct it to the vacuoles. If such sequences are absent, DNA encoding targeting sequences may be operatively linked to the clone.

20 Any clone that encodes or that has been modified to encode a protein that has invertase activity as defined herein may be used for preparing DNA constructs and transferred into an appropriate host plant.

In particular, DNA encoding residues 1-636 of a 25 tomato fruit invertase preproprotein having the amino acid sequences set forth in Seq. ID No. 1 have been isolated. In addition, genomic DNA clones encoding both *L. esculentum* and *L. pimpinellifolium* invertase (Seq. ID Nos. 2 and 4, respectively) are provided.

30 Those of skill in the art recognize that, by virtue of the degeneracy of the genetic code, numerous DNA molecules have nucleic acid sequences that encode the amino acid sequence set forth in Seq. ID No. 1. For example, a presently preferred nucleic acid sequence is 35 set forth in Seq. ID No. 1, corresponding to the native

-25-

nucleotide sequence encoding tomato fruit invertase from *L. esculentum*. Other sequences of nucleotides that encode this invertase or an invertase that functions equivalently may be obtained by methods known to those of
5 skill in the art, including chemical synthesis and isolation of other invertase-encoding genes. Such invertases are limited to those that function in tomatoes and catalyze the hydrolysis of sucrose to fructose and glucose. If the invertase is not directed to the plant
10 vacuole or is improperly processed in the tomato plant, DNA sequences encoding proper signal and vacuolar targeting sequences should be operatively linked to the invertase-encoding DNA.

Full-length cDNA and genomic clones that encode
15 tomato fruit vacuolar invertase from both *L. esculentum* and *L. pimpinellifolium* have been isolated. The coding regions of both genes are identical. The promoter and other upstream regions of the genomic clones that encode the *L. pimpinellifolium* and *L. esculentum* invertases
20 include repetitive regions. Each repeat unit includes the sequence 5'-TATTTAAT-3', which matches known plant nuclear protein binding sites. The *L. pimpinellifolium* repetitive region includes an additional repeat unit and differs at two other sites from the *L. esculentum*
25 repetitive region.

Invertase gene expression in *L. esculentum* differs significantly from that in *L. pimpinellifolium*. For example, analysis of total RNA isolated from various stages of fruit development revealed that, in *L.*
30 *pimpinellifolium*, invertase mRNA appears in green fruit, and is present at high levels in pink and red fruit. In *L. esculentum* cv. UC82, however, invertase mRNA does not appear until the pink stage of fruit development and is present at high levels only in red fruit. The apparent
35 differences in fruit solids content may result from

-26-

differences in gene expression, due to *cis*-acting factors, including the differences in nucleotide sequences of regulatory regions associated with the invertase genes, or regulatory factors acting in *trans*,
5 such as factors which induce the earlier expression of the invertase gene in *L. pimpinellifolium*.

The promoter region from the *L. pimpinellifolium* invertase gene can be fused to DNA encoding invertase and introduced into *L. esculentum* tomato plants in order to
10 produce *L. esculentum* plants in which invertase is expressed at an earlier stage in ripening than in the non-transgenic plants. Constructs in which the promoter region from the *L. pimpinellifolium* invertase gene is fused to the *L. esculentum* invertase gene have been
15 prepared as means for altering expression of the *L. esculentum* invertase gene and to thereby increase the soluble solids content of the fruit.

Thus, the designed pattern of expression of the invertase gene in transgenic tomato plants may be
20 accomplished by operatively linking it to a developmentally regulated promoter. DNA encoding developmentally regulated regulatory sequences obtained from the invertase gene and sequences that direct proper secretion and targeting of invertase have been identified
25 and isolated, and DNA constructs containing DNA encoding invertase and fruit-specific genomic regulatory sequences are provided.

Selection of developmentally regulated promoters and other regulatory sequences.
30 **Identification and isolation of promoter regions.**
To accomplish the modification of invertase gene expression in tomato plants by transformation of tomato tissue with DNA encoding invertase, such DNA has been fused to developmentally responsive promoters. Preferred
35 promoter regions and other regulatory sequences are those that are fruit specific and developmentally controlled.

-27-

Such preferred regulatory regions include those that promote expression of recombinant invertase at an earlier stage of tomato fruit development than occurs when the subject plant does not express recombinant invertase.

- 5 Other embodiments include regulatory sequences that promote expression throughout fruit development.

Any developmentally regulated promoter region that, when linked to invertase-encoding DNA and introduced into a tomato plant host, does not promote expression until 10 early in fruit ripening and promotes expression at high levels early during fruit ripening, is preferred for use herein. Especially preferred regulatory sequences are those which promote expression at about the breaker stage 15 of tomato fruit development, the stage at which the fruit begins to turn pink or red, with continued promotion of expression until the tomato fruit has reached the red stage.

More specifically, regulatory regions have been isolated by screening a *L. pimpinellifolium* genomic DNA 20 library with a probe containing cDNA encoding all or a portion of an invertase-encoding DNA sequence. A preferred subclone is one, as can be identified by restriction enzyme-mapping, that includes the 5' portion 25 of an invertase-encoding sequence because there is a good chance that it will hybridize with the ATG start-site and upstream sequences of genomic clones.

For example, a 0.8-kb *Xba*I-*Hind*III 5'-end fragment of pTOM3-L1 was used as a cDNA probe and a plasmid containing an invertase-encoding fragment was isolated 30 from an *L. pimpinellifolium* genomic DNA library. Such selected positive clones may be plaque-purified and restriction enzyme-mapped. Restriction enzyme-mapped clones having inserts extending the furthest upstream of the translation start site are then chosen for further 35 characterization as the most likely to include the

-28-

desired promoter sequences. For example, clone λPI.6, which is a preferred clone described herein, include about 4 kb upstream of the translation start site.

Developmentally regulated promoter regions may also 5 be isolated by any method known to those of skill in the art. For example, a method for isolating clones that encode a portion of a developmentally regulated gene is described in PCT Application WO 89/12230, which is based on U.S. Patent Application Serial No. 07/352,658 to 10 Fitzmaurice et al., filed May 18, 1989, which is herein incorporated in its entirety by reference. The method provides a means to isolate promoter regions from genes that are, preferably, expressed in the tomato fruit prior to ripening, at the breaker stage. Use of this method is 15 also described in the Examples herein. Any method by which developmentally regulated clones may be identified and isolated may be used.

The selected clones can be further characterized by northern analysis to select those that hybridize to mRNAs 20 abundant at the developmental stage selected for study. For example, those that hybridize to mRNA that exhibits the desired developmentally regulated expression may be used as probes to screen genomic libraries in order to isolate the gene and regulatory sequences. The upstream 25 portions can be sequenced and promoter regions identified and tested by fusing to reporter genes and looking for the appropriate regulation or pattern of expression in transgenic plants.

In particular, one such clone has been used to isolate 30 a developmentally regulated promoter. This clone, which, upon expression *in vitro* yields a ~50 kDa translation product, that exhibits regulated expression during fruit ripening, has been used to screen an *L. esculentum* tomato genomic library and to isolate hybridizing clones. 35 One such clone appears to encode a protein that has

-29-

substantial homology with bacterial histidine decarboxylase and is herein referred to as the HDC gene. The portion of the clone upstream from the translation initiation site has been isolated and includes the 5 promoter region, which appears to be a developmentally regulated promoter.

One such promoter region that has been selected, herein referred to as the *L. esculentum* HDC promoter region, is among those preferred for use herein. DNA 10 fragments that include nucleotides from about 1 to about 888 or 889 of Seq. ID No. 3, or that are substantially homologous thereto and encode a developmentally regulated promoter are herein referred to as the HDC promoter. All 15 or a portion of this region which promotes developmentally regulated expression is operatively linked to DNA encoding invertase. Constructs including this promoter region in operative linkage with DNA 20 encoding invertase have been prepared. The constructs, HDC/3-L1.1, HDC/3-L1.2 and HDC/3-L1.3, contain different portions of the upstream sequences and are used to prepare transgenic plants. Such transgenic plants should express developmentally regulated levels of invertase.

In other preferred embodiments, invertase gene regulatory sequences from *L. esculentum* and 25 *L. pimpinellifolium* are provided. These have been obtained by constructing genomic libraries of each species and screening them with a probe made from an invertase-encoding clone, such as plasmid pTOM3-L1, selected from a *L. esculentum* fruit cDNA library. The 30 positive clones have been restriction enzyme-mapped and partially or completely sequenced. Thus characterized, the regulatory regions from these DNA fragments have been used to make fusions with invertase-encoding sequences. Thus *L. pimpinellifolium* promoter sequences can be 35 fused to *L. esculentum* invertase-encoding regions.

-30-

- Other developmentally regulated promoters may be identified and isolated by means known to those of skill in the art. Such promoters preferably confer fruit specificity and an appropriate temporal control upon the expression of the coding sequences to which they are fused. For example, U.S. Patent No. 4,943,674 to Houck et al. describes methods and examples of developmentally regulated promoter regions, such as the 2A11 promoter.
- Preferred promoter regions are fruit-specific developmentally regulated promoter regions, including, but not limited to, the promoter region from *L. pimpinellifolium* and *L. esculentum*, the HDC promoter, the polygalacturonase promoter, and the 2A11 gene.
- Most preferred promoter regions for use herein include the HDC promoter region (Seq. ID No. 3) and the regulatory regions from the *L. pimpinellifolium* genomic clone (Seq. ID No. 4).
- Invertase gene promoter regions and other developmentally regulated promoter regions may also be linked to heterologous genes for developmentally regulated expression of genes of interest in plants. The regulatory regions, including the promoters, may be linked to other genes to achieve regulated expression of such genes in plants. For example, constructs have been prepared in which different portions of the HDC promoter region and the *Lycopersicon* invertase promoter regions have been fused to the coding region of the *E. coli* β -glucuronidase (GUS) gene.
- Finally, invertase encoding DNA may be operatively linked to a constitutive promoter, such as the CaMV 35S promoter, and introduced into a plant. DNA constructs containing the CaMV 35S promoter have been constructed and used to prepare transgenic plants. By virtue of constitutive expression of the exogenous invertase in

-31-

addition to expression of the endogenous invertase gene, invertase levels in the plant should increase. The resulting transgenic fruit should exhibit increased soluble solids content.

5 **Identification and isolation of DNA encoding processing and targeting signals.**

In addition to appropriate promoter selection, other regulatory sequences, including vacuolar targeting sequences must be included in the DNA construct in order 10 to effect proper targeting of the heterologous invertase.

The identification and isolation of regulatory elements associated with tomato fruit vacuolar invertase genes can be accomplished by use of a cDNA clone encoding invertase as a probe. In addition, such sequences may 15 be prepared synthetically and linked to DNA encoding an invertase that lacks such sequences.

DNA encoding sequences of amino acids that direct targeting or sorting of the invertase protein, as well as other proteins, to the tomato fruit vacuoles are 20 provided. These include signal sequences, such as the invertase signal sequence, and carboxyl-terminal propeptide sequences. A 15 amino acid glycosylated carboxyl-terminal propeptide (CTPP) of the barley lectin proprotein is necessary for the efficient sorting of this 25 protein to plant cell vacuoles [Bednarek et al. (1990) *The Plant Cell* 2:1145-1155]. In addition, it appears that the β -1,3-glucanase CTPPs of *Nicotiana tabacum* and *N. plumbaginifolia* may also be necessary for vacuolar sorting. Sequence comparison between the *Nicotiana* β - 30 1,3-glucanase CTPPs and the carboxyl-terminal domain of the vacuolar tomato fruit invertase indicates 85% sequence similarity over a region of seven amino acids between residues 607 and 613 of tomato fruit invertase-encoding regions (see Seq. ID No. 1). Vacuolar 35 targeting sequences, thus, may include DNA that encodes residues 607-613 of Seq. ID No. 1 and any additional

-32-

portions of Seq. ID No. in that region necessary to effect vacuolar targeting.

- DNA encoding tomato fruit invertase signal sequences and other sequences that are removed during processing
5 are also provided. This region of the structural gene includes nucleotides encoding amino acids 1 through about 92 of the invertase-encoding Seq. ID No. 1. This DNA, as well as DNA identified as the carboxyl-terminal sequences (including residues 607-613 of Seq. ID No. 1)
10 of the precursor protein described above, may also be used to direct the targeting of homologous or heterologous peptides into vacuoles by host recombinant solanaceous plants. Expression of the desired homologous or heterologous peptides from DNA constructs that include
15 the above-described signal sequences and carboxyl-terminal coding sequences upstream of, and downstream of, respectively, and in reading frame with, the peptide, should direct a substantial portion of the expressed protein into the vacuoles of the host plant. Thus,
20 invertase-encoding genes from sources other than tomato fruit, such as yeast, may be linked to DNA encoding the CTTP and DNA encoding the signal sequence from tomato invertase, thereby directing the gene product to the vacuole.
25 The DNA encoding invertase and constructs herein provided may also be introduced into a variety of hosts, such as solanaceous plants, prokaryotic or eukaryotic hosts, and invertase encoded by such DNA may be expressed and isolated. Exemplary hosts include yeast, fungi,
30 mammalian cells, insect cells, and bacterial cells. The use of such hosts for the recombinant production of heterologous genes is well known in the art. In preferred embodiments, the DNA constructs are introduced into tomato plants and expressed by transgenic tomato
35 plants during fruit development.

-33-

Introduction of heterologous DNA into plants.

The DNA constructs provided herein are introduced into plants, plant tissues, or into plant protoplasts, particularly tomato plants, plant tissues, and

5 protoplasts, to produce transgenic tomato plants.

Numerous methods for producing or developing transgenic plants are available to those of skill in the art. The method used is primarily a function of the species of plant. These methods include, but are not limited to, the use of vectors, such as the modified Ti plasmid system of *Agrobacterium tumefaciens*, the Ri plasmid system of *Agrobacterium rhizogenes* and the RNA virus vector, satellite tobacco mosaic virus (STMV).

10 Other methods include direct transfer of DNA by processes such as PEG-induced DNA uptake, microinjection, electroporation, microprojectile bombardment, and direct and chemical-induced introduction of DNA [see, e.g., Uchimiya et al. (1989) *J. Biotech.* 12: 1-20 for a review of such procedures].

15 The resulting plants are grown, and fruits and seeds may be harvested. The transgenic plants may then be cross-bred in order to produce plants and seeds that are homozygous for the transgenic DNA. Such plants and seeds are contemplated for use herein.

20 25 The following examples are included for illustrative purposes only and are not intended to limit the scope of the invention.

EXAMPLE 1

**CHARACTERIZATION OF INVERTASE PURIFIED FROM *L.*
30 *ESCULENTUM* FRUIT.**

A. Identification of a ~52 kDa protein as invertase.

Gel analysis of samples of invertase purified from *L. esculentum* fruit by ammonium sulfate precipitation of the supernatant of a crude homogenate followed by DEAE-cellulose, Sephadryl S-200 and Concanavalin A-Sepharose column chromatography, revealed sequential enrichment of

-34-

a major protein having an apparent molecular weight of ~52 kDa and two minor species of about 30 and 24 kDa.

Polyclonal antisera reactive against carrot cell wall invertase were used to identify the ~52 kDa protein isolated from *L. esculentum* fruit as invertase. The antisera, described by Lauriere et al. [(1988) *Biochimie* 70:1483-1491], also reacted with the ~30 and ~24 kDa proteins.

The predominant ~52 kDa protein present in purified preparations of *L. esculentum* fruit vacuolar invertase, as well as the two minor additional proteins (~30 and ~24 kDa) detected in these preparations, were subjected to N-terminal protein sequence analysis. The ~52 kDa protein and the ~24 kDa protein contain identical residues at the N-terminus (22 residues); the ~30 kDa protein yielded a 22-amino acid sequence that was different from the sequence of N-terminal residues obtained from the ~52 and ~24 kDa proteins. Subsequent analysis of the amino acid sequence deduced from a full-length invertase cDNA clone pTOM3-L1 (Example 2B) confirmed that the 22-residue sequence representing the N-terminus of the ~30 kDa protein is contained within the intact ~52 kDa protein.

Analysis of purified *L. esculentum* invertase showed that the ~52 kDa protein hydrolyzed sucrose to glucose and fructose and that it hydrolyzed raffinose to melibiose and fructose.

Invertase activity and substrate specificity were assayed by reacting 3.8 µg of protein obtained following Concanavalin A-Sepharose column chromatography with 90 mg/ml of substrate (sucrose or raffinose), in 13.6 mM citric acid and 26.4 mM NaHPO₄ (pH 4.8) at 30°C for 30 minutes. The reaction was stopped with the alkaline copper reagent of Somogyi [(1945) *J. Biol. Chem.* 160:51-68] and the liberated reducing sugars were measured according to Nelson [(1944) *J. Biol. Chem.*.

-35-

153:375-380]. To analyze substrate activity, the products of these reactions were subjected to thin layer paper chromatography using isobutanol:pyri-dine:H₂O:acetic acid (12:6:4:1) as the solvent for ascending chromatography [Gordon et al. (1962) *J. Chromatog.* 8:44]. The positions of the carbohydrates were detected with alkaline silver nitrate [Chaplin (1986) "Monosaccharides", in *Carbohydrate Analysis, A Practical Approach*, Chaplin and Kennedy, eds; IRL Press, 10 Washington, DC, pp. 1-36].

This characterization, in addition to the invertase activity assay results and the cross-reactivity to carrot invertase antibody, and protein sequence analysis confirmed identification of the ~52 kDa protein as *L. esculentum* invertase.

B. Identification of ~52 kDa protein as vacuolar invertase

Invertase activities in protoplasts and vacuoles were evaluated and the purified invertase protein was compared to vacuolar proteins.

Protoplasts and vacuoles were purified from *L. esculentum* fruit tissue by squeezing two ripened tomato fruit into 35 ml of 25 mM Tris-MES [2-(N-morpholino)ethanesulfonic acid], pH 6.5, containing 0.7 M mannitol [Low pH Buffer; Boudet and Alibert (1987) *Methods in Enzymology* 148:74-81] and filtering the resulting suspension through two pieces of cheese cloth and stainless steel mesh (30 mesh). The filtrate was centrifuged at 100 x g for 3 min to collect protoplasts. The protoplasts were then resuspended in the same buffer and collected by centrifugation at 100 x g for 3 min.

Vacuolar fractionation was accomplished by a modification of the procedure described by Boudet and Alibert (1987) *Methods in Enzymology* 148:74-81. The protoplast fraction was diluted 1:4 with 20% (w/v) Ficoll in Low pH Buffer, then overlaid with 5 ml of Low pH

-36-

Buffer containing 6 mg/ml DEAE-dextran and 10% (v/v) Ficoll, 2 ml of 6 mg/ml dextran sulfate (potassium salt) and 5% (v/v) Ficoll in 25 mM Tris-MES, pH 8.0, containing 0.7 M mannitol (High pH Buffer), and 2 ml of 1.2 mg/ml dextran sulfate and 1% (v/v) Ficoll in High pH Buffer followed by centrifugation at 2000 x g for 30 min. Vacuoles were recovered from the interface between the 5% and 1% Ficoll layers.

Protoplasts and vacuoles were lysed in the presence 10 of invertase assay buffer and analyzed for invertase activity, as described above. The results of invertase assays of vacuolar and protoplast lysates revealed that the invertase activity in the vacuolar fraction was ~16-fold higher than the invertase activity in the 15 protoplasts.

To determine if the vacuolar form of invertase was the form of invertase purified from *L. esculentum* fruit tissue, total protein from the purified vacuoles was subjected to SDS-PAGE and subsequent immunoblot analysis 20 with the carrot invertase-specific antisera. The ~52 kDa, ~30 kDa, and ~24 kDa proteins detected in invertase purified from tomato fruit were detected in the vacuolar proteins.

C. Production of polyclonal antisera to *L. Esculentum* 25 vacuolar invertase.

Polyacrylamide gel-purified *L. esculentum* fruit vacuolar invertase (~52 kDa species obtained following separation on Concanavalin A-Sepharose) was excised from a gel, and 75 to 100 µg of protein were injected into 30 rabbits, three times at intervals of two weeks, for the production of antibodies. The immunoglobulin fraction from immunized rabbits was subsequently purified from raw antiserum by Protein A-Sepharose affinity column chromatography. To remove antibodies reactive with 35 glycans, the immunoglobulin fraction of this antiserum was passed over a horseradish peroxidase-Sepharose column

-37-

which was prepared by coupling horseradish peroxidase to CNBr-activated Sepharose 4B (Pharmacia LKB Biotechnology, Piscataway, NJ).

The antibodies reactive with tomato fruit invertase 5 peptides did not bind to the column and the resulting "cleared" antibody fraction reacted specifically with tomato fruit invertase.

EXAMPLE 2

ISOLATION OF cDNA ENCODING *L. ESCULENTUM* VACUOLAR INVERTASE.

A. Library construction.

Total RNA was isolated from fresh *L. esculentum* cv. UC82 (grown from seeds obtained from Dr. Charles Rick, University of California at Davis, Dept. of Vegetable Crops) 3-inch intermediate fruit (i.e., fruit at the "turning" to "pink" stage of development) as described by De Vries et al. [(1988) In *Plant Molecular Biology Manual*, S.B. Gelvin, R.A. Schilperoort, and D.P.S. Verma, eds., Kluwer Academic Publishers, Dordrecht, The Netherlands, pp. B6:1-13]. Poly(A)⁺ RNA was isolated from total RNA by oligo(dT)-cellulose chromatography (mRNA Purification Kit, Pharmacia LKB Biotechnology, Piscataway, NJ).

The poly(A)⁺ RNA was used to construct size-selected 25 cDNA libraries (of ~0.6 - 2 kb and ~2 - 4 kb and greater) in λgt11. cDNA synthesis was carried out by the method of Lapeyre and Amalric [(1985) Gene 37:215-220] with the following modifications. A NotI-oligo(dT) primer-adapter (Promega Corporation, Madison, WI) was used in first-strand synthesis. The addition of EcoRI adapters was followed by digestion with NotI, generating cDNA inserts with a NotI site at the polyadenylated end and an EcoRI site at the opposite end. The cDNA was size-fractionated on a Sepharose CL-4B column. cDNAs of approximately 0.6 - 2 kb and 1.2 - 4 kb or greater in length were ligated 35 into λgt11 Sfi-Not (Promega Corporation, Madison, WI)

-38-

which had been digested with EcoRI and NotI. The cDNA-containing λgt11 vectors were then packaged and amplified (Gigapack^R II Gold Packaging Kit, Stratagene Cloning Systems, La Jolla, CA).

5 **B. Library screening.**

To identify clones expressing tomato invertase, the immunological screening protocol described in Sambrook et al. [(1989) *Molecular Cloning: A Laboratory Manual*, Vol. 2, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp. 12.16-12.20] was used to screen directionally cloned *L. esculentum* fruit cDNA expression libraries. The primary antibody was antisera raised against tomato invertase protein and cleared of anti-glycan antibodies (see Example 1), and was pretreated as follows: 250 μl each of *E. coli* strain Y1090 extract and crude λgt11-*E. coli* strain Y1090 lysate were added to 5 ml of a 1:10 dilution of the tomato invertase antisera in the blocking buffer (described in the screening protocol), and the mixture was incubated 4 h at room temperature, then diluted 1:100 in blocking buffer. The secondary antibody was an anti-rabbit IgG-alkaline phosphatase (AP) conjugate (Promega Corporation, Madison, WI), diluted 1:7500 as described in the screening protocol.

25 Approximately 250 immunopositive plaques were detected in the primary screen of approximately 300,000 plaques. Six positive clones were plaque-purified by standard methods. The inserts of three of these clones, ranging from ~1.1 to 1.5 kb in size, were subcloned into the *Sfi*I and *Not*I sites of vector pGEM-11zf(-) (Promega Corporation, Madison, WI). Plasmid mini-preps were performed according to the protocol of Sambrook et al. [(1989) *Molecular Cloning: A Laboratory Manual*, Vol. 1, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, p.1.40].

-39-

The insert DNAs were sequenced according to the USB Sequenase® (United States Biochemical Corporation, Cleveland, Ohio) protocol. The complete sequence of the longest of the clones, pTOM3, contains 1339 bp which 5 correspond to bases 840-2163 in Seq. ID No. 1, plus a poly(A) tail which has 15 adenine residues. Several classes of cDNA clones were identified, based on the location of the poly(A) tail.

Comparison of the deduced amino acid sequence of the 10 insert in pTOM3 and the amino acid sequences of peptides generated by CNBr cleavage of the gel-purified preparation of *L. esculentum* vacuolar invertase revealed that a portion of the deduced amino acid sequence is present in one of the sequenced peptides.

15 The N-terminal protein sequence determined by sequencing the predominant ~52 kDa protein of partially purified preparations of *L. esculentum* fruit vacuolar invertase was not located in the pTOM3-deduced amino acid sequence, indicating that this cDNA clone does not encode 20 a full-length invertase mRNA.

A 0.5 kb HindIII fragment of pTOM3, containing the 5' half of the DNA insert, was used as a probe to re-screen both the large insert (approximately 1.2 up to >4 kb) and small insert (~0.6-2.0 kb) λgt11 *L. esculentum* 25 cv. UC82 fruit cDNA expression libraries for full-length invertase cDNA clones, essentially according to the procedure of Maniatis et al. [(1982) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp.320-321, 326-328]. The 30 filters were washed for 15 min each, once at 42°C in 2X SSC, 0.1% SDS, once at 42°C in 1X SSC, 0.1% SDS, once at 42°C in 0.5X SSC, 0.1% SDS, and once at 65°C in 0.1X SSC, 0.1% SDS.

35 Eleven hybridizing clones were plaque purified. The insert sizes of these clones ranged from ~1.4 to ~2.2 kb.

-40-

Inserts from several of these clones were subcloned and sequenced as described above. The longest clone, pTOM3-L1, is 2199 bp in length (see, Seq. ID No. 1), encodes full-length tomato invertase, and also contains an 5 additional 21 bp relative to pTOM3 preceding the poly (A) tail.

Comparison of the 3' ends of all of the *L. esculentum* cDNA clones sequenced revealed five classes of clones, based on the location of the poly(A) tail, at 10 either the site indicated in Seq. ID No. 1, or a relative position of -23, -21, -17, or +13. All overlapping sequences were identical, except at a site 37 bp upstream of the beginning of the poly(A) tail in pTOM3-L1. That site contains a pyrimidine in all cases, C in 8 of 9 15 clones and T in the other clone.

Comparison of the amino acid sequence deduced from pTOM3-L1 with the amino acid sequences of peptides generated by CNBr cleavage of vacuolar invertase purified from *L. esculentum* fruit and the amino-terminal sequence 20 of purified invertase indicated that the protein encoded by this protein is invertase. In addition, sequence analysis of the ~30 kDa and ~24 kDa proteins which reacted strongly with anti-carrot invertase antisera in 25 immunoblots of purified *L. esculentum* vacuolar invertase suggests that these proteins are degradation products of the mature invertase protein. The first 22 amino acids of the ~24 kDa protein were determined by sequence analysis to be identical to the first 22 amino acids of the ~52 kDa protein. The first 22 amino acids of the ~30 30 kDa protein were determined by sequence analysis and did not correspond to the amino terminus of *L. esculentum* fruit vacuolar invertase. The first 22 amino acids of the ~30 kDa putative degradation product of tomato invertase are identical to amino acids 253-274 deduced 35 from the nucleotide sequence of pTOM3-L1 (Seq. ID No. 1).

-41-

The ATG translation start signal of pTOM3-L1 is the only in-frame ATG that results in an open reading frame from which a single peptide including all of the amino acid sequences derived from purified *L. esculentum* fruit vacuolar invertase can be deduced. Amino terminal sequence analysis of purified *L. esculentum* fruit vacuolar invertase indicates that the mature protein begins at the tyrosine residue at position 93 relative to the methionine encoded by the translation start codon (Seq. ID No. 1). Therefore, it appears that the first 92 amino acids of the protein encoded by pTOM3-L1 are co- or post-translationally cleaved, leaving a sequence of 544 amino acids extending from the amino terminus of the mature protein to the residue encoded by the codon preceding the stop codon.

Computer-assisted analysis of the resulting 544 amino acid peptide indicates that it has a molecular weight of ~60 kDa. The molecular weight of the mature deglycosylated tomato fruit vacuolar invertase was estimated to be ~45 kDa by SDS-PAGE. It is possible that additional post-translational modifications of the 636 amino acid precursor protein occur at the carboxyl terminus.

Based upon the assumption that the molecular weight of the mature protein is ~45 kDa, the carboxyl terminus of the mature protein has been predicted to be at amino acid position 502. This prediction is based upon the apparent molecular weight of the mature protein estimated by SDS-PAGE and thus is subject to experimental error of ±10 amino acids.

EXAMPLE 3

ISOLATION OF A cDNA ENCODING *L. PIMPINELLIFOLIUM* VACUOLAR INVERTASE.

A cDNA expression library was prepared from orange fruit of *L. pimpinellifolium* Trujillo, La Libertad Perù (grown from seeds obtained from Dr. Charles Rick,

-42-

University of California at Davis, Dept. of Vegetable Crops) and was screened essentially as described in Example 2, except that the initial screen used ^{32}P -labeled *L. esculentum* cDNA clone pTOM3 as a probe. Five clones

5 were identified, plaque purified, subcloned, and sequenced. The longest clone (pLP-19) contained an insert which is 30 bp shorter than the pTOM3-L1 insert at the 5' end and 7 bp longer at the 3' end prior to the poly(A) tail.

10 To isolate a full-length cDNA clone that encodes *L. pimpinellifolium* invertase, the *L. pimpinellifolium* fruit cDNA expression library was re-screened using a ^{32}P -labeled synthetic oligonucleotide complementary to nucleotides 7-33 of the *L. esculentum* cDNA (see Seq. ID

15 NO. 1). Hybridization was carried out overnight at 42°C in 50% formamide, 5X SSPE, 5X Denhardt's solution, 0.1% SDS, 200 $\mu\text{g}/\text{ml}$ denatured salmon sperm DNA and $10^6 \text{ cpm}/\text{ml}$ radiolabeled probe. Several of the hybridizing clones were purified and characterized and compared with cDNA

20 pTOM3-L1. *L. pimpinellifolium* clone pPIM11 was determined to be a full-length invertase-encoding cDNA that contains 7 nucleotides at the 5' end that are not present at the 5' end of pTOM3-L1 and 17 fewer nucleotides preceding the poly(A) tail than pTOM3-L1.

25 Clone pPIM11 extends seven nucleotides farther in the 5' untranslated sequence direction than pTOM3-L1; the overlapping portions of the 5' ends of pPIM11 and pTOM3-L1 are identical.

The nucleotide sequences of the *L. pimpinellifolium* 30 cDNA clones are essentially identical to those of the *L. esculentum* cDNA clones, differing only slightly at the 3' end. Several classes of *L. pimpinellifolium* cDNA clones with 3' ends of differing lengths were identified, as was the case for the *L. esculentum* clones. The *L.*

35 *pimpinellifolium* cDNA poly(A) tails begin either at the

-43-

same site as in *L. esculentum* clone pTOM3-L1 (see, Seq. ID No. 1) or at a relative position of -21, -17, or +7, and overlapping regions are identical in all clones. The site comparable to the variable site 37 bp upstream of 5 the pTOM3-L1 poly(A) tail also contains a pyrimidine in all the *L. pimpinellifolium* cDNA clones, except that it is a T in 6 of the 7 clones sequenced and a C in only one clone. No other differences were found between the vacuolar invertase cDNAs of the two species.

10

EXAMPLE 4

ISOLATION OF *L. PIMPINELLIFOLIUM* VACUOLAR INVERTASE GENE PROMOTER REGIONS.

A. Construction of a genomic library.

Genomic DNA was isolated from seedling tissue of *L. 15 pimpinellifolium* Trujillo, LaLibertad Perù (grown from seeds obtained from Dr. Charles Rick, University of California at Davis, Dept. of Vegetable Crops) according to the procedure of Rogers and Bendich [(1988) *Plant Molecular Biology Manual*, pp. A6/1-10, Kluwer Academic Publishers, S. B. Gelvin, R. A. Schilperoort, eds.].
20 Restriction enzyme fragments generated by partial digestion with Sau3AI were cloned into λFIX™ II (Stratagene, La Jolla, CA) according to manufacturer's instructions. The ligation reaction was packaged using 25 Stratagene Gigapack™ II Gold packaging extracts.

B. Library screening.

A 0.8 kb *Xba*I-*Hind*III restriction enzyme fragment from plasmid pTOM3-L1 (a clone encoding invertase from the *L. esculentum* fruit cDNA library), see Example 2B, 30 was labeled with ³²P. This probe was used to screen the *L. pimpinellifolium* genomic library as described in Example 2, except that the wash in 0.5X SSC, 0.1% SDS was omitted. Two of the 12 positive clones, λPI.1 and λPI.3, were selected for further characterization.

35 The *L. pimpinellifolium* genomic library was then rescreened by the method described above with the ³²P-

-44-

labeled, gel-purified ~0.8 kb *Xba*I-*Hind*III fragment from the 5' end of the pTOM3-L1 insert. Six positive clones were selected for further characterization. Clone λ PI.6 was determined to encode the largest amount of sequence 5' 5' from the initiation ATG.

C. DNA sequencing.

Restriction enzyme fragments of the insert of λ PI.6 were subcloned and sequenced by the dideoxynucleotide 10 chain termination method, using Sequenase^R (United States Biochemical Corporation, Cleveland, Ohio). The sequenced region, provided in Seq. ID No. 4, includes the promoter and protein-encoding regions of the *L. pimpinellifolium* tomato vacuolar invertase gene.

15 The *L. pimpinellifolium* genomic sequence including the promoter and protein-encoding regions is set forth in Seq. ID No. 4. The transcription start site was identified by primer extension analysis by the method of Sambrook et al. [(1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., Vol. 1, pp. 7.79-7.83]. The oligonucleotide primer used in the primer extension 20 reaction is complementary to nucleotides 74-107 of SEQ ID No. 1.

25 The transcription start site is located at nucleotide position 3668 of Seq. ID No. 4. The TATA box appears to be located at nucleotide positions 3637 through 3640. The translation start site appears to begin at nucleotide position 3686, and the stop codon 30 begins at nucleotide position 7609. In addition, the cDNA 3' end sequences of different lengths share 100% sequence identity with the comparable regions of the genomic sequence. The variable site located near the 3' end of the cDNAs contains a T in the genomic clones 35 sequenced.

-45-

EXAMPLE 5

ISOLATION OF *L. ESCULENTUM* INVERTASE GENE PROMOTER REGIONS.

A. Construction of genomic library.

5 A genomic library was constructed in λ FIXTM II using DNA isolated from seedling tissue of *L. esculentum* cv. UC82 (grown from seeds obtained from Hunt-Wesson Foods, Inc., Pasadena, CA), according to the procedure described in Example 4.

10 B. Library screening.

The insert of plasmid pTOM3 (see Example 2) was labeled with ^{32}P and used as a probe to screen the *L. esculentum* genomic library as described in Example 4. Four clones containing putative invertase-encoding 15 sequences were identified, and three were selected for further characterization.

C. DNA sequencing.

Restriction fragments of the insert of the above genomic clones were subcloned and sequenced. The 20 sequenced regions, provided in Seq. ID No. 2, include the promoter and protein-encoding regions of *L. esculentum* tomato vacuolar invertase gene.

The *L. esculentum* genomic sequence including the promoter and protein-encoding regions is set forth in 25 Seq. ID No. 2. The transcription start site is located at nucleotide position 3502. The TATA box appears to be located at nucleotide positions 3471 through 3474. The translation start site appears to begin at nucleotide position 3520, and the stop codon begins at nucleotide 30 position 7443. The cDNA 3' end sequences of different lengths share 100% identity with the comparable region of the genomic sequence. The variable site located near the 3' end of the cDNAs contains a C in the genomic clones sequenced.

-46-

EXAMPLE 6

PREPARATION OF CONSTRUCTS CONTAINING TOMATO INVERTASE
GENE PROMOTERS AND/OR CODING REGIONS.

5 A. *L. pimpinellifolium* invertase promoter/invertase gene
constructs.

Plasmid PI.6/BIN was constructed by inserting DNA containing regulatory and protein-encoding regions of the *L. pimpinellifolium* invertase gene into pBIN19 [Bevan (1984) *Nucl. Acids Res.* 12:8711-8721; Clontech, Palo Alto, CA.], a vector containing DNA sequences required for transferring DNA to plant cells. PI.6/BIN contains the *L. pimpinellifolium* invertase gene coding region as well as 3.7 kb of upstream and 3.4 kb of downstream sequence (nucleotides 1-10965 in Seq. ID No. 4).

15 Plasmid PI.6/BIN was constructed in two steps: (1) the ~7.8 kb insert DNA purified from plasmid pPI.6B7.8, which includes part of the *L. pimpinellifolium* invertase gene and ligated with BamHI-digested plasmid, pPI.6BgB2.9, which includes the remainder of the invertase gene, to yield a third plasmid; and (2) the ~10.7 kb insert, which includes nucleotides 1-10965 of Seq. ID No. 4 and 18 additional nucleotides (EcoRI, SalI, XbaI polylinker) at the 5' end, was purified from an EcoRI/BamHI (partial) digest of the plasmid and ligated 25 with EcoRI- and BamHI-digested pBIN19 (Clontech, Palo Alto, CA) to yield PI.6/BIN.

20 B. *L. esculentum* invertase promoter/invertase gene constructs.

Plasmid pEI.23/BIN was constructed by inserting DNA 30 containing regulatory and protein-encoding regions of the *L. esculentum* invertase gene into pBIN19. Plasmid pEI.23/BIN contains the *L. esculentum* invertase gene coding region as well as 3.5 kb of upstream and 3.4 kb of downstream sequences (nucleotides 1-10798 in Seq. ID No. 35 2).

-47-

Plasmid pEI.23/BIN was constructed in two steps: (1) a ~7.8 kb BamHI insert was purified from a plasmid, pEI.3B7.8, which includes a portion of the the *L. esculentum* invertase gene and then ligated to a BamHI-digested plasmid, pEI.2BB2, which contains the remainder of the gene, to produce a third plasmid, pEI.23BgB10.7, from which the ~10.7 kb insert was purified from an EcoRI/BamHI (partial) digest of the plasmid; and (2) the purified fragment (nucleotides 1-10798 in Seq. ID No. 2 with the polylinker at the 5' end), was ligated to EcoRI- and BamHI-digested pBIN19 to yield pEI.23/BIN.

C. *L. esculentum* invertase promoter/GUS gene constructs.

DNA from the promoter region of the *L. esculentum* gene between 3 base pairs and either 747, 913, or 1079 base pairs upstream from the initiator ATG from pEI.23BgB10.7 (Example 6B) corresponding to sequences between nucleotides 3517 and either 2773, 2607, and 2441 in Seq. ID No. 2 was amplified by the polymerase chain reaction (PCR) using Seq. ID No. 5 as a first 20 oligonucleotide primer, which created an XbaI site 1 bp upstream of the initiator ATG, and Seq. ID No. 6 as a second primer (located in the region of direct repeats), which created a HindIII site 752 bp, 918 bp, 1084 bp and possibly additional sites upstream of the initiator ATG. 25 These multiple priming sites are due to the presence of six 166-bp tandem direct repeats in this promoter.

The PCR products were digested with HindIII and XbaI and ligated with HindIII- and XbaI-digested pBI221 (Clontech, Palo Alto, CA) to fuse the promoter sequences 30 with the GUS gene coding sequence in pBI221. Two correct plasmids, EI2GUS715 and EI2GUS1100, were identified by the production of ~750 bp and ~1100 bp fragments, respectively, upon digestion with HindIII and XbaI.

-48-

Plasmid EI2GUS715 was digested with EcoRI and HindIII, and the 3.1 kb fragment was ligated with EcoRI- and HindIII-digested pBIN19 to produce EI2GUS715BIN.

- The 3.4 kb EcoRI-HindIII fragment of plasmid
5 EI2GUS1100 was ligated into pBIN19 by the same procedure used for EI2GUS715 to produce plasmid EI2GUS1100BIN.

EXAMPLE 7

TRANSFORMATION OF TOMATO PLANTS WITH INVERTASE PROMOTER CONSTRUCTS.

10 A. Transformation of *L. esculentum* seedlings.

The transformation of seedlings of *L. esculentum* cv. UC82 (grown from seeds obtained from Ferry Morse Seed Co., Modesto, CA) was done essentially according to the protocol of Fillatti et al. [(1987) *Bio/Technology* 5:726-15 730]. Plasmids PI.6/BIN and EI.23/BIN (Example 6) were inserted into *Agrobacterium tumefaciens* strain LBA4404 [Clontech, Palo Alto, CA] through triparental mating [Ditta, G. (1986) *Meth. Enzymol.* 118] for transfer into *L. esculentum* seedlings.

20 The cultures were incubated at 27°C with 16 hours of light per day under 4,000 lux of light intensity. When kanamycin-resistant shoots reached a height of one inch, they were rooted on rooting medium, which is identical to regeneration 2Z medium except that it lacks hormones and 25 contains 250 µg/ml cefotaxime and 50 µg/ml kanamycin. The transgenic shoots are grown into fruit-bearing transgenic tomato plants.

B. Assays for recombinant gene expression.

Tomato fruit tissues are assayed for invertase or
30 GUS expression at various stages of fruit development. Invertase activity is determined according to the assay described in Example 1. GUS activity is determined essentially according to the protocol of Jefferson [(1987) *Plant Mol. Biol. Rep.* 5:387-405].
35 Protein concentration is determined according to the

-49-

Protein Assay using reagents obtained from Bio-Rad Laboratories (Richmond, CA).

EXAMPLE 8

CONSTRUCTION OF HDC PROMOTER CONSTRUCTS

5

A. Isolation of a developmentally regulated gene.

1. Construction of cDNA library.

Tomato fruit at the 3-inch intermediate stage was collected from greenhouse-grown *L. esculentum* cv. UC82 (grown from seeds obtained from Hunt-Wesson Foods, Fullerton, CA) and frozen in liquid nitrogen. Polysomes were prepared from 10 g of pulverized frozen tissue [Schröder et al. (1976) *Eur. J. Biochem.* 67:527-541] and RNA was extracted from the polysomes using an SDS-phenol-chloroform procedure similar to that described by Palmiter [(1974) *Biochemistry* 13:3606-3615] and stored at -70°C. Poly(A)+ RNA was selected by affinity chromatography on oligo(dT)-cellulose columns using the procedure of Aviv and Leder [(1972) *Proc. Natl. Acad. Sci. USA* 69:1408-1412], except that LiCl was used instead of NaCl.

A cDNA library was prepared by methods similar to those reported by Villa-Komaroff et al. [(1978) *Proc. Natl. Acad. Sci. USA* 75:3727-3731]. The cDNA molecules were made double-stranded with DNA polymerase I, Klenow fragment (New England BioLabs, Beverly, MA). To insure completion of the second strand synthesis, the DNA molecules were incubated with reverse transcriptase (Molecular Genetic Resources, Tampa, FL). The double-stranded molecules were made blunt-ended by digestion with S1 nuclease (Boehringer Mannheim Biochemicals, Indianapolis, IN) and tailed with d(C) using terminal transferase (Ratliff Biochemicals, Los Alamos, NM).

The tailed DNAs were annealed to pBR322 DNA which had been digested at the *Pst*I site and tailed with d(G) (New England Nuclear, Boston, MA). The recombinant

-50-

plasmid DNA molecules were used to transform LE392 *E. coli* cells which were then plated on LB-tetracycline (15 µg/ml) plates. The resultant cDNA library was stored by the procedure of Hanahan and Meselson [(1980) *Gene* 10:63-5 67].

2. Library screening.

The cDNA library was screened to identify clones containing insert sequences which were expressed either constitutively or under developmental regulation. To achieve this, "early" and "late" stage RNA probes were prepared, labeled in a polynucleotide kinase reaction, and hybridized with the filter-bound DNAs.

a. Preparation of probes.

Total RNA was prepared from 1-inch green "early" and 3-inch intermediate "late" *L. esculentum* cv. UC82 fruit and subjected to oligo-dT cellulose chromatography for the selection of poly(A)+ RNA essentially as described by Aviv and Leder [(1972) *Proc. Natl. Acad. Sci. USA* 69:1408-1412], but using LiCl for the binding instead of NaCl.

Poly(A)+ RNA prepared from early and late stages of *L. esculentum* cv. UC82 tomato fruit development was fractionated on a linear 5-20% sucrose gradient, and samples of RNA from gradient fractions were translated in an mRNA-dependent rabbit reticulocyte translation system by the method of Pelham and Jackson [(1976) *Eur. J. Biochem.* 67:247-256] to produce peptides labeled with L-(³⁵S)-methionine [New England Nuclear (Boston, MA); October 1979 Manual]. Protein synthesis was assayed by determining the incorporation of TCA-precipitable label [Pelham and Jackson (1976) *Eur. J. Biochem.* 67:247-256], and the translation products were analyzed by electrophoresis on a 12.5% SDS acrylamide gel [Laemmli (1970) *Nature* 227:680-685] and fluorography.

35 b. Library screening.

-51-

Replica filters were prepared and the plasmids amplified [Hanahan and Meselson (1980) *Gene* 10:63-67] using 200 µg/ml chloramphenicol. DNA from cDNA clones was denatured, neutralized, and fixed to 150 mm
5 nitrocellulose filters [Maniatis et al. (1982) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York].

RNAs from a gradient fraction of one-inch green (early) RNA encoding proteins with a molecular mass of
10 ~30 - ~60 kDa and from a similar gradient fraction of three-inch intermediate (late) RNA were labeled with ³²P in a polynucleotide kinase (Boehringer-Mannheim, Milwaukee, WI) reaction. These labeled fruit RNAs were then hybridized to approximately 10,000 cDNA clones (a
15 fraction of the complete cDNA library) bound to nitrocellulose filters. Of 313 clones which yielded strong hybridization signals, 36% contained insert sequences which appeared to be expressed differentially at the two different stages of development.

20 3. Identification of clone ptomUC82-3 as encoding a developmentally regulated protein.

Plasmid DNA was prepared from clones which yielded strong hybridization signals, labeled with ³²P by nick translation and was used to probe northern blots of
25 "early" and "late" fruit RNAs.

Total RNA was prepared from 1" green and 3" intermediate developmental stages of UC82 fruit as described above. RNA blots were prepared essentially as described by Thomas [(1980) *Proc. Natl. Acad. Sci. USA* 77:5201-5205], and separate panels of RNA were hybridized with ³²P-labeled insert DNA from six cDNA clones. The autoradiographic patterns of hybridization indicated that clone ptomUC82-3 encodes a developmentally regulated, fruit-specific sequence which hybridized to a
30 single RNA band with an apparent mobility of ~1.7 kb on a
35 1.5% agarose gel. These northern hybridization data, as

-52-

well as hybridization/selection analyses, indicated that cDNA clone ptomUC82-3 corresponds to a gene which is expressed at low levels at early stages of fruit ripening, high levels at intermediate fruit ripening
5 stages, and decreased levels in fully ripened fruit. The insert in ptomUC82-3, which was restriction-enzyme mapped and sequenced by the dideoxynucleotide chain termination method, was less than full-length cDNA clone but did contain an ATG start codon.

10 B. Isolation of the tomato HDC promoter.

A genomic library was constructed in λ FIXTMII (Stratagene, La Jolla, CA) using DNA isolated from seedling tissue of *L. esculentum* cv. UC82, as described in Example 4A. The genomic library was screened with a
15 32 P-labeled probe prepared from the 0.8 kb insert purified from cDNA ptomUC82-3 following digestion with *Pst*I. The screening conditions were identical to those described in Example 2B and clones which hybridized to the probe were identified and plaque-purified.

20 One of the clones isolated from the genomic DNA library, λ UC82-3.3, containing nucleic acids 1-4032 of Seq. ID No. 3, was shown by restriction enzyme mapping to contain putative regulatory regions upstream of the translation start site. A 3.7 kb *Sst*I-*Bgl*III fragment
25 from the 5' end of this clone was subcloned. Sequence analysis of the insert of this subclone revealed that it contains six exons that have 95-100% identity with comparable positions of cDNA ptomUC82-3 and appears to include a promoter region. A fragment containing the
30 remaining 347 nt upstream from the *Sst*I restriction site near the 5' end of the λ UC82-3.3 insert was subcloned and sequenced.

The results of a sequence similarity search through the GenBank database release 67.0 and EMBL database
35 release 26.0 [Devereaux et al. (1984) *Nucl. Acids Res.*

-53-

12:387-395] indicate a 60% similarity between the amino acid sequences predicted from cDNA clone ptomUC82-3 and the *Morganella morganii* bacterial histidine decarboxylase gene.

5 The promoter-containing region of λUC82-3.3, nucleotides 1-888 of Seq. ID No. 3, is herein referred to as the HDC promoter.

c. **HDC promoter/tomato fruit invertase constructs**

1. **HDC/3-L1.1.**

10 Construct HDC/3-L1.1 contains 538 bp of the HDC promoter region from λUC82-3.3 (nucleotides 349 to 886 of Seq. ID No. 3) fused to the *L. esculentum* cv. UC82 invertase cDNA pTOM3-L1 insert (nucleotides 1 to 2199 of Seq. ID No. 1), which is fused at the 3' end to the NOS (nopaline synthase) terminator.

15 pTOM3-L1 was digested with *Xba*I, made blunt-ended with T4 DNA polymerase, then digested with *Not*I to yield a 2202 bp fragment containing 3 nucleotides from the vector polylinker (AGC) plus the complete *L. esculentum* cv. UC82 invertase cDNA coding sequence (nucleotides 1 to 2199 of Seq. ID No. 1).

20 The above fragment from pTOM3-L1, the fragment containing the HDC promoter (nucleotides 349 to 886 of Seq. ID No. 3) were purified and ligated with *Not*I-, 25 *Sst*I-digested pGEM-11zf(-) (Promega Corporation, Madison, WI). The resulting plasmid was called -540/3-L1.

25 The NOS terminator is contained in plasmid pBI101 (Clontech, Palo Alto, CA). Plasmid pBI101 was digested with *Sst*I and *Hind* III and made blunt-ended with T4 DNA 30 polymerase yielding an ~10 kb vector fragment. The purified vector fragment was ligated to the DNA insert of -540/3-L1, which had been prepared by digestion with *Not*I and *Sst*I and made blunt-ended with T4 DNA polymerase, to produce construct HDC/3L-1.1.

35 2. **HDC/3-L1.2.**

-54-

Construct HDC/3-L1.2 is identical to HDC/3-L1.1 except that it contains 886 bp of the HDC promoter region from λUC82-3.3 rather than 538 bp. Construct HDC/3-L1.2, thus, contains 886 bp of the HDC promoter region from 5 λUC82-3.3 (nucleotides 1 to 886 of Seq. ID No. 3) fused to the tomato invertase gene (nucleotides 1 to 2199 of Seq. ID No. 1), which is fused at the 3' end to the NOS (nopaline synthase).

3. HDC/3-L1.3.

10 Construct HDC/3-L1.3 is identical to HDC/3-L1.1 except that it contains 690 bp of the HDC promoter region from λUC82-3.3 rather than 538 bp. Construct HDC/3-L1.3, thus, contains 690 bp of the HDC promoter region from 15 λUC82-3.3 (nucleotides 1 to 690 of Seq. ID No. 3) fused to the *L. esculentum* cv. UC82 invertase cDNA (nucleotides 1 to 2199 of Seq. ID No. 1) which is fused at the 3' end to the NOS (nopaline synthase) terminator.

D. HDC-promoter/GUS constructs.

1. HDC/GUS.1.

20 Construct HDC/GUS.1 contains a promoter fragment from λUC82-3.3 which extends from 794 to 3 bp upstream of the ATG start codon (nucleotides 94 to 886 in Seq. ID No. 3) fused to the *E. coli* GUS gene.

25 Plasmid pUC82-3.3NH was digested with *Dde*I, the ends of the resultant fragment were filled in with Klenow DNA polymerase, and the 792 bp fragment was isolated and purified. Plasmid pUC82-3.3NH was constructed by inserting the 3.4 kb restriction enzyme fragment, which extends from the *Not*I site in the vector polylinker to 30 the first *Hind*III site from the 5' end of the λUC82-3.3 insert, into the *Not*I and *Hind*III sites of pGEM-11zf(-) (Promega Corporation, Madison, WI) to produce pUC82-3.3NH.

Plasmid pBI101.3/pUC was made by inserting the 2200 35 bp *Eco*RI-*Hind*III fragment of pBI101.3 (Clontech, Palo

-55-

Alto, CA) into *EcoRI-HindIII*-digested pUC119 [Vieira and Messing (1987) In *Methods in Enzymology*, R. Wu and L. Grossman, Eds., Vol. 153, pp. 3-11, Academic Press, New York]. The 792 bp fragment was ligated to pBI101.3/pUC which had been digested with *HindIII* and *BamHI*, and the resulting plasmid was called -790/GUS.

The 3 kb *EcoRI-HindIII* fragment containing the HDC promoter-GUS fusion was isolated from -790/GUS and ligated to *EcoRI*- and *HindIII*-digested pBIN19 to produce 10 HDC/GUS.1.

2. HDC/GUS.2

Construct HDC/GUS.2 contains 690 bp of the HDC promoter region from λUC82-3.3 (nucleotides 1 to 690 of Seq. ID No. 3) fused to the *E. coli* GUS gene.

15 Plasmid pUC82-3.3NH was digested with *XbaI* and *SspI*, and the 710 bp fragment was isolated and purified. The 710 bp fragment was ligated to purified *XbaI*- and *SmaI*-digested pBI101.3/pUC to create -690/GUS.

The 2.9 kb *EcoRI-HindIII* fragment containing the HDC 20 promoter-GUS fusion was isolated from -690/GUS and ligated to *EcoRI*- and *HindIII*-digested pBIN19 to produce HDC/GUS.2.

EXAMPLE 9

**TRANSFORMATION OF *L. ESCULENTUM* WITH HDC PROMOTER
25 CONSTRUCTS AND ANALYSIS FOR RECOMBINANT GENE EXPRESSION.**

The transformation of seedlings grown from *L. esculentum* cv. UC82 seeds was performed essentially by the protocol of Fillatti et al. [(1987) *Bio/Technology* 5:726-730], as described in Example 7.

30 Invertase and GUS expression in the fruit of transformed tomato plants may be assayed as described in Example 7.

EXAMPLE 10

INVERTASE C-TERMINAL/GUS CONSTRUCTS

35 Two constructs have been assembled using the signal and targeting sequences from secreted proteins. The

-56-

first of these constructs (35S/GUS44) was assembled to express a fusion protein with the signal sequence from phytohemagglutinin-L (PHA) fused to the amino-terminus of *E. coli* GUS and was designed to allow GUS to be targeted 5 to the endoplasmic reticulum and then secreted. The second construct (35S/GUS-INV) incorporates the C-terminus of tomato fruit vacuolar invertase into GUS and should target GUS to the vacuole.

35S/GUS44 was constructed from plasmid pA35/PHIN44 10 [Dickinson et al. (1991) *Plant Physiol.* 95:420-525]. The yeast invertase coding sequence in pA35/PHIN44 was replaced by the GUS coding sequence of plasmid pGUSN358-S (Clontech, Palo Alto, CA) by digesting pA35/PHIN44 with *Sph*I and ligating this vector with a *Sph*I-digested 15 fragment derived from PCR amplification of plasmid pGUSN358-S, using Seq. ID No. 7, which anneals to the 5' end of the GUS gene coding sequence, and Seq. ID No. 8, which anneals to the 3' end of the GUS gene coding sequence, as primers.

20 The 1.8 kb fragment obtained after PCR amplification of pGUSN358-S was digested with *Sph*I and ligated into pA35/pHIN44 to produce plasmid 35S/GUS44. This plasmid contains the following noteworthy features: 25 1) a cauliflower mosaic virus promoter, CaMV 35S, for high-level expression; 2) the coding sequence for the first 44 amino acids of PHA-L which includes the 20 amino acid signal sequence for efficient translocation across the ER membrane; 3) the GUS reporter protein coding sequence fused in-frame with the PHA sequence and 30 modified by deletion of a glycosylation site that allows GUS to move through secretory system; 4) a unique *Pst*I restriction site which immediately precedes the termination codon of GUS for in-frame C-terminal fusions; and 5) an octopine synthase transcriptional terminator. 35 Upon introduction of this construct into a plant, active

-57-

GUS which is secreted by the default pathway to the plant cell wall should be produced.

To demonstrate the ability of the C-terminus of tomato invertase to target heterologous proteins to the 5 vacuole, the coding sequences for the last 39 amino acids of tomato invertase (amino acids 598-636 in Seq. ID No. 1) were fused in-frame to the 3' end of the GUS gene contained in plasmid 35S/GUS44.

First, plasmid 35S/3L-1b was constructed to place 10 the OCS transcriptional terminator after the invertase cDNA sequence and to thereby facilitate subsequent steps. Plasmid pTOM3-L1 was digested with *Not*I, filled in with Klenow DNA polymerase, digested with *Xba*I, and the 2.2 kb fragment was purified and cloned into the CaMV 35S 15 promoter/OCS terminator vector pA35. Plasmid pA35 was prepared for this cloning by digesting with *Sph*I, filling-in with Klenow DNA polymerase, and then digesting with *Sal*I. The resulting clone was named 35S/3L-1b and was used for PCR amplification of the 3' end of the 20 invertase sequence.

For amplification of a fragment containing the 3' end of the 35S/3L-1b insert, a synthetic oligonucleotide was designed which included a new *Pst*I restriction site to facilitate the in-frame fusion of GUS and invertase 25 sequences. The sequence of one primer was Seq. ID No. 9. The second primer was the pUC/M13 reverse primer (New England Biolabs, Inc., Beverly, MA). Amplification by PCR was conducted according to the procedure of Perkin-Elmer/Cetus (Norwalk, CT). The resultant 600 bp fragment 30 was then digested with *Pst*I and *Hind*III and ligated into 35S/GUS44, which had been digested with *Pst*I and *Hind*III and purified, to produce plasmid 35S/GUS-INV.

These constructs are transformed into tomato tissue by methods described in Example 7. The resulting

-58-

transformed plants are then assayed for GUS activity as described in Example 7.

EXAMPLE 11

CaMV 35S PROMOTER/TOMATO FRUIT INVERTASE CONSTRUCTS

5 A. 35S/3-L1/BIN Overproducing construct.

1. Construction.

The cDNA sequence encoding tomato fruit vacuolar invertase (nucleotides 1-2199 of Seq. ID No. 1) was inserted between the CaMV 35S promoter and the nopaline synthase (NOS) terminator in vector pCAMVCN (Pharmacia LKB Biotechnology, Piscataway, NJ). Plasmid pCAMVCN was digested with *Pst*I, blunt-ended with T4 DNA polymerase, purified, and ligated with the purified 2202 bp *Xho*I-*Not*I fragment of pTOM3-L1, which was also made blunt-ended with T4 polymerase. The resulting clone, named 35S/3-L1, was ligated into pBIN19 as a cassette fragment containing the CaMV 35S promoter, the invertase cDNA sequence, and the NOS terminator, to produce 35S/3-L1/BIN. This subcloning was performed by digesting 35S/3-L1 at the 3' end with *Bgl*II and at the 5' end with a partial *Xba*I digestion. The 3.0 kb fragment was purified and ligated into pBIN19 prepared by digestion with *Xba*I and *Bam*HI.

2. Transformation and expression.

Seedlings grown from seeds of *L. esculentum* cv. UC82 were transformed with 35S/3-L1/BIN essentially by the protocol of Fillatti et al. [(1987) *Bio/Technology* 5:726-730], as described in Example 7. To determine the level of invertase activity in plants generated from the transformed seedlings, mature leaf tissue from the transgenic plants and control non-transgenic plants that had been growing in soil for two months was assayed as follows. Tissue samples (1 g) were homogenized in a mortar and pestle with 2 ml homogenization buffer (0.25 M Tris phosphate, pH 7.6, containing 1 mM EDTA and 5 mM DTT). All steps were performed at 4°C. Homogenates were

-59-

centrifuged for 10 min at 14,000 x g and the supernatant was stored on ice. Leaf extracts were adjusted to contain equal concentrations of protein, which were determined by the Bradford Reagent method (BioRad Laboratories, Richmond, CA). Samples of the leaf extracts were analyzed in invertase activity gels, which were performed according to the method of Gabriel and Wang [(1969) *Anal. Biochem.* 27:545-554], as modified by Carlson et al. [(1981) *Genetics* 98:25-40]. Purified tomato fruit invertase was used as a positive control in these assays.

Tomato plants transformed with 35S/3-L1/BIN were shown to contain high levels of invertase activity in their leaves. With the conditions used for the extraction and assay, no invertase activity was detected in extracts from non-transgenic tomato leaves.

B. Antisense construct 35/3-L1(-).

An antisense invertase construct designed to reduce expression of vacuolar invertase in tomato fruit has been prepared. The vacuolar tomato fruit invertase clone pTOM3-L1 cDNA insert (nucleotides 1-2199 of Seq. ID No. 1) was inserted into the CaMV 35S promoter/terminator cassette in the reverse orientation to create 35S/3-L1(-). pTOM3-L1 was digested with *NotI*, blunt-ended, digested with *XhoI*, and the 2202 bp fragment was purified and cloned into pA35 prepared by digestion with *SmaI* and *SalI*. 35S/3-L1(-) contains the CaMV 35S promoter fused to an antisense pTOM3-L1 cDNA and the OCS transcriptional terminator. This fusion construct was ligated as an *EcoRI-SstI* fragment into the corresponding sites of pBIN19 to yield plasmid 35S/3-L1(-)BIN.

C. Cosuppression construct 35S/3-L1(P).

A construct for use in cosuppression of endogenous invertase expression was constructed by removing a coding segment from 35S/3-L1 to create a construct 35S/3-L1(P)

-60-

which encodes a truncated, nonfunctional protein. To prepare construct 35S/3-L1(P), 35S/3-L1 was digested with *Pst*I, which digests at two sites (nucleotides 1205 and 1386 in Seq. ID No. 1) within the invertase coding region, and religated. This produced a 181 bp deletion, creating a shift in the reading frame after codon 400 in Seq. ID No. 1 and the introduction of a stop codon four codons downstream.

Using the same strategy as described above for 10 35S/3-L1/BIN, 35S/3-L1(P) was mobilized into pBIN19 as an *Xba*I fragment (obtained following a partial digestion) to create 35S/3-L1(P)BIN.

Transgenic plants that contain this construct should express reduced levels of invertase compared to a non- 15 transgenic plant of the same species.

Since modifications will be apparent to those of skill in the art, it is intended that this invention be limited only by the scope of the appended claims.

-61-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: NOVEL INVERTASE GENE(S) AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 9

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: Patentin Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

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 (B) FILING DATE: 22-FEB-1991

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(A) APPLICATION NUMBER: US 07/771,331
 (B) FILING DATE: 04-OCT-1991

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(A) TELEPHONE: 619-552-1311

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..1917
- (D) OTHER INFORMATION: /product= "L. esculentum vacuolar invertase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTATT ATG GCC ACT CAG TGT TAT GAC CCC GAA AAC TCC GGC TCT CGT	48
Met Ala Thr Gln Cys Tyr Asp Pro Glu Asn Ser Ala Ser Arg	
1 5 10	

TAC ACA TTA CTC CCG GAT CAA CCC GAT TCC GGC CAC CGG AAG TCC CTT	96
Tyr Thr Leu Leu Pro Asp Gln Pro Asp Ser Gly His Arg Lys Ser Leu	
15 20 25 30	

-62-

AAA ATC ATC TCC GGC ATT TTC CTC TCC GTT TTC CTT TTG CTT TCT GTA Lys Ile Ser Gly Ile Phe Leu Ser Val Phe Leu Leu Ser Val 40 45	144	35
GCC TTC TTT CCG ATC CTC AAC AAC CAG TCA CCG GAC TTG CAA ATC GAC Ala Phe Phe Pro Ile Leu Asn Asn Gln Ser Pro Asp Leu Gln Ile Asp 50 55 60	192	
TCC CGT TCG CCG GCG CCG CCG TCA AGA GGT GTT TCT CAG GGA GTC TCC Ser Arg Ser Pro Ala Pro Pro Ser Arg Gly Val Ser Gln Gly Val Ser 65 70 75	240	
GAT AAA ACT TTT CGA GAT GTA GCC GGT GCT AGT CAC GTT TCT TAT GCG Asp Lys Thr Phe Arg Asp Val Ala Gly Ala Ser His Val Ser Tyr Ala 80 85 90	288	
TGG TCC AAT GCT ATG CTT AGC TGG CAA AGA ACG GCT TAC CAT TTT CAA Trp Ser Asn Ala Met Leu Ser Trp Gln Arg Thr Ala Tyr His Phe Gln 95 100 105 110	336	
CCT CAA AAA AAT TGG ATG AAC GAT CCT AAT GGA CCA TTG TAT CAC AAG Pro Gln Lys Asn Trp Met Asn Asp Pro Asn Gly Pro Leu Tyr His Lys 115 120 125	384	
GGA TGG TAC CAC CTT TTT TAT CAA TAC AAT CCA GAT TCA GCT ATT TGG Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Asp Ser Ala Ile Trp 130 135 140	432	
GGA AAT ATC ACA TGG GGC CAT GCT GTA TCC AAG GAC TTG ATC CAC TGG Gly Asn Ile Thr Trp Gly His Ala Val Ser Lys Asp Leu Ile His Trp 145 150 155	480	
CTC TAC TTG CCT TTT GCC ATG GTT CCT GAT CAA TGG TAT GAT ATT AAC Leu Tyr Leu Pro Phe Ala Met Val Pro Asp Gln Trp Tyr Asp Ile Asn 160 165 170	528	
GGT GTC TGG ACA GGG TCC GCT ACC ATC CTA CCC GAT GGT CAG ATC ATG Gly Val Trp Thr Gly Ser Ala Thr Ile Leu Pro Asp Gly Gln Ile Met 175 180 185 190	576	
ATG CTT TAT ACC GGT GAC ACT GAT GAT TAT GTG CAA GTG CAA AAT CTT Met Leu Tyr Thr Gly Asp Thr Asp Asp Tyr Val Gln Val Gln Asn Leu 195 200 205	624	
GCG TAC CCC GCC AAC TTA TCT GAT CCT CTC CTT CTA GAC TGG GTC AAG Ala Tyr Pro Ala Asn Leu Ser Asp Pro Leu Leu Leu Asp Trp Val Lys 210 215 220	672	
TTC AAA GCC AAC CCG GTT CTG GTT CCT CCA CCC GGC ATT GGT GTC AAG Phe Lys Gly Asn Pro Val Leu Val Pro Pro Pro Gly Ile Gly Val Lys 225 230 235	720	
GAC TTT AGA GAC CCG ACT ACT GCT TGG ACC GGA CCA CAA AAT GGG CAA Asp Phe Arg Asp Pro Thr Thr Ala Trp Thr Gly Pro Gln Asn Gly Gln 240 245 250	768	
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GTT TAT GAA ACT TCC AAC TTC ACA AGC TTT AAG CTA TTG GAT GGA GTG Val Tyr Glu Thr Ser Asn Phe Thr Ser Phe Lys Leu Leu Asp Gly Val 275 280 285	864	
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CCG GTA TCT ACT AAA AAA ACA AAC GGG TTG GAC ACA TCA TAT AAC GGG Pro Val Ser Thr Lys Lys Thr Asn Gly Leu Asp Thr Ser Tyr Asn Gly 305 310 315	960	
CCG GGT GTA AAG CAT GTG TTA AAA GCA AGT TTA GAT GAC AAT AAG CAA Pro Gly Val Lys His Val Leu Lys Ala Ser Leu Asp Asp Asn Lys Gln 320 325 330	1008	
GAT CAT TAT GCT ATT GGT ACG TAT GAC TTG GGA AAG AAC AAA TGG ACA Asp His Tyr Ala Ile Gly Thr Tyr Asp Leu Gly Lys Asn Lys Trp Thr 335 340 345 350	1056	

-63-

CCC GAT AAC CCG GAA TTG GAT TGT GGA ATT GGG TTG AGA CTA GAC TAT Pro Asp Asn Pro Glu Leu Asp Cys Gly Ile Gly Leu Arg Leu Asp Tyr 355 360 365	1104
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AGA GTA CTG TGG GGA TGG ATT GGG GAA ACT GAC AGT GAA TCT GCT GAC Arg Val Leu Trp Gly Trp Ile Gly Glu Thr Asp Ser Glu Ser Ala Asp 385 390 395	1200
CTG CAG AAG GGA TGG GCA TCT GTA CAG AGT ATT CCA AGG ACA GTG CTT Leu Gln Lys Gly Trp Ala Ser Val Gln Ser Ile Pro Arg Thr Val Leu 400 405 410	1248
TAC GAC AAG AAG ACA GGG ACA CAT CTA CTT CAG TGG CCA GTG GAA GAA Tyr Asp Lys Lys Thr Gly Thr His Leu Leu Gln Trp Pro Val Glu Glu 415 420 425 430	1296
ATT GAA AGC TTA AGA GTG GGT GAT CCT ACT GTT AAG CAA GTC GAT CTT Ile Glu Ser Leu Arg Val Gly Asp Pro Thr Val Lys Gln Val Asp Leu 435 440 445	1344
CAA CCA GGC TCA ATT GAG CTA CTC CGT GTT GAC TCA GCT GCA GAG TTG Gln Pro Gly Ser Ile Glu Leu Leu Arg Val Asp Ser Ala Ala Glu Leu 450 455 460	1392
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GCT AGC AGA GGC ATT TTG GGA CCA TTT GGT GTC ATA GTA ATT GCT GAT Ala Ser Arg Gly Ile Leu Gly Pro Phe Gly Val Ile Val Ile Ala Asp 495 500 505 510	1536
CAA ACG CTA TCT GAG CTA ACG CCA GTT TAC TTT TAC ATT TCT AAA GGA Gln Thr Leu Ser Glu Leu Thr Pro Val Tyr Phe Tyr Ile Ser Lys Gly 515 520 525	1584
GCT GAT GGT CGT GCA GAG ACT CAC TTC TGT GCT GAT CAA ACT AGA TCC Ala Asp Gly Arg Ala Glu Thr His Phe Cys Ala Asp Gln Thr Arg Ser 530 535 540	1632
TCT GAG GCT CCG GGA GTT GGT AAA CAA GTT TAT GGT AGT TCA GTC CCT Ser Glu Ala Pro Gly Val Gly Lys Gln Val Tyr Gly Ser Ser Val Pro 545 550 555	1680
GTG TTG GAC GGT GAA AAA CAT TCA ATG AGA TTA TTG GTG GAT CAC TCA Val Leu Asp Gly Glu Lys His Ser Met Arg Leu Leu Val Asp His Ser 560 565 570	1728
ATT GTG GAG AGC TTT GCT CAA GGA GGA AGA ACA GTC ATA ACA TCG CGA Ile Val Glu Ser Phe Ala Gln Gly Gly Arg Thr Val Ile Thr Ser Arg 575 580 585 590	1776
ATT TAC CCA ACA AAG GCA GTA AAT GGA GCA GCA CGA CTC TTT GTT TTC Ile Tyr Pro Thr Lys Ala Val Asn Gly Ala Ala Arg Leu Phe Val Phe 595 600 605	1824
AAC AAT GCC ACA GGG GCT AGC GTT ACT GCC TCC GTC AAG ATT TGG TCA Asn Asn Ala Thr Gly Ala Ser Val Thr Ala Ser Val Lys Ile Trp Ser 610 615 620	1872
CTT GAG TCA GCT AAT ATT CAA TCC TTC CCT TTG CAA GAC TTG TAATCTTCTT Leu Glu Ser Ala Asn Ile Gln Ser Phe Pro Leu Gln Asp Leu 625 630 635	1924
TATTCGTTT TTTTTTCTT TTTCATTGAG GTTATTTC ACCGACGTCC CATCAAGAAA	1984
GGGAAGAGGG AGATCAATAT ATGTAGTGT ATTCCCCATA CCTTAGGATT AGATGTCATC	2044

-64-

TAGCAATGTC AAATCTAGTA GAGTATACAA TGTATGGTT CCTGGAAACC GAGTAGAGCT	2104
TACCTGGATT CTATGAAAC TAAGAAAAGCT CAGCAAATAT ATGCACAAAT AATTTACAGA	2164
AACAACTTGG GAATGTTGAC AAAAAAAA AAAAA	2199

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum*

(ix) FEATURE:

- (A) NAME/KEY: precursor RNA
- (B) LOCATION: 3520..7445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCTCGATA AGTTATGTCT TGTTGGAATC GATATCAAT AACCGTCGAC GGATCTTTG	60
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CACTTAGAAA AGTGACATT TGGAATGGTA GTCCATAAT CAAGGTATAA TGTCAGTGGG	240
GTACAATAA ATTATTATGT GATAGTATAA CCGTAAGATA TCAAATACGG TTGTCGCTT	300
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GATGCAATGA GGTTTGTGTT GATCTGGCA CATATGAAA ACTTGAATGC ATGTAATGAA	420
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GATCTCAAA GAAGGATAAG AGTTTCTGG TGATGAAACT CTATCTGGT GCAATGAGGG	840
CACTAGTGCA TCTTACTAAC AATATTTGAC TAGATATTG TTGTCAGTA AATTTACTGG	900
CAAGATTCAAG TTTCTCCCCG ATAAAAGGAC ATTGAAATGG TGTTGAGCAC ATGAATGAAT	960
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CACCATATTC AAGAAATGTG TGGTTTTCT TTAAAAAAAG AATATACCAA CCACAATGTA	1260
CAAAGATTGG AGACATCATC ACAAGAACATC AAGTGATGTT TTAATCAGGG GGAGTACAAT	1320
ACCGCGTTGCA CTCTTTTCCC CTTGATCGAG GTTCTTTCCC CACTGGATTCT TCCGACAAG	1380
GTTTTTAATG AGGCAACAAA TGGTGGCGTAT CAAAGATAT GTGTAATCTT TTCTTTCAC	1440
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ACATCCAAGG GGGAGTGTAA TAAATACATT GAATTAAGTG GATAGTCAT AAGGTTGGCA	1560

-65-

CATGAAACAC CATTCAATT CACTAGGTGA CATGAACCTT TTGGATAAG AATGTATCTA	1620
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GTTCAATTCACT TATTGTAATA TATACATATG AGACTGAA ACACGTGAAT AGGAAGAAAG	1740
TCTTATCTTC CACTTCACTT CTCTGTCTT CTCTCTTAT GATTATATTC TTATGAGCTT	1800
GATTTTATAA CACGAATCTC ATTATACGAA AAGTTTACT ATTTATATT AATTAATAGA	1860
GGATTTAACAC TTTTTAAATT TCTGTCTTTA TAGATGAGAA CTGTCTTT TGTTGAATCC	1920
AACAAACAT TCAATGAAGA CAAATCAACC TGAAATCCC TTTCAGTAG GATTTATTGCG	1980
AATCTCATTA TACGAAAAGT TTACTATTAT ATTAAATT AATAGAGGAT TAAACTTTT	2040
TAATTTCTG TCTTTATAGA TGAGAACTTG TCCTTTGTT GAATCCAAC AACATTCAA	2100
TGAAGACAAA TCAACCTGTA AATCCCTTC AAGTAGGATT TATCGAACTC TCATTATAGC	2160
AAAAGTTTA CTATTTATAT TTAATTAATA GAGAATTAA ACTTTTAAAT TTCTGTCTT	2220
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CTGTAAATC CCTTCAGT AGGATTATT CGAATCTCAT TATACGAAA GTTTACTAT	2340
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TCAAGTAGGA TTATTCGAA TCTCATTATA CGAAAAGTT TACTATTAT ATTAAATTAA	2520
TAGAGAATT AAACCTTTA AATTCGTC TTATAGATG AGAACTTGTC TTTTGTGA	2580
ATCCAACCTAA ACATTCAATG AATACAATC AACCTGTAAC TCCCTTCAA GTAGGATTAA	2640
TTCGAATCTC ATTATACGAA AAGTTTACT ATTATATTAT ATTAAATAGA GAATTTAAC	2700
TTTTAAATT TCTGTCTTTA TAGATGAGAA CTGTCTTT TGTTGAATCC AACTAAACAT	2760
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TTTACATTCC ACATTTAAAT CTATAATGAA AGTTACTAA ATATACTATC AAGGAGAAAA	2940
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ACTGACCTAA TAACAGTTT TATTTGAGC AAGAAAAGTA GTAAATTTG TAAATAAAG	3240
AACCAAATA AATCATTITA ATCAAAGTAA AATATAATAA CGATTAAAT AAGTATACA	3300
TAAAGTCATT TCAATGAAGT GAAATAATG AAGAAGTAA ATAAAAAAT TAACCAAACA	3360
GTAAGCAGTAC TTTGGTCAT TTCTCTAA CCCAAGTGTA CCTCAAATTAA TAAAGTCCT	3420
TTGGTTACTC AATTCGTTG GTCCAGTC TTTCTGTGT TCAATCACCTA TATATATAGC	3480
AGTAGACTAG TAGCTCTC CATTCTCTA TCTCTCTTAA TGCCCACTCA GTGTATGAC	3540
CCCGAAAACCT CCCTCTCTCG TTACACATTA CTCCCGGATC AACCCGATTC CGGCCACCGG	3600
AAGTCCCTTA AAATCATCTC CGGCATTTTC CTCTCCGTTT TCTCTTGCT TTCTGTAGCC	3660
TTCTTCCGA TCTCAACAA CCAGTCACCG GACTTGCAAA TCGACTCCCG TTGCGCCGGCG	3720
CCGGCGTCAA GAGGTGTTTC TCAGGGAGTC TCCGATAAAA CTTTTGAGA TGTAGCCGGT	3780
GCTAGTCACG TTCTTATGC GTGGTCAAAT GCTATGCTTA GCTGGCAAAG AACGGCTTAC	3840
CATTTCAAC CTCAAAAAAA TTGGATGAAC GGTAAATTAAAC TTCTTATTT TGACTTTCT	3900

-66-

TTAATTCCTT TTTTATTGAGAATTAAATT GAAATTATTATAAAATCTT ATAACAGTTC	3960
TTTTTTCTT CAATGATATT TATGGCTATT GATCTGTTGG GGGTATCTTT TGGATTCTGA	4020
TTGGATGCTA TTCTGCAGAT CCTAATGGTG AGTTCAAAGT TAATTATTAT CACTATTTC	4080
TGCTAGTTT TAATTAATTA TATTCTAACTATGATTAACTTTAAAGCAATCTCAT	4140
GAATGAGCAA ATCATTAAATT CGGGTGCTTA TGATATCAT CTGGTTAAT CCTTTACCT	4200
TATACTCAA AACAAATATT ACTCCCTCA AAATAATTGA TGTTTGACAT AATCAATGTG	4260
ATGTTAATT TTTTTCTT CAAATTGCG CCTTCTAAC CCCTATAATG ATTATGTCAA	4320
ATCCAAGTG AAAAGACTAT CATAATTACA TATGCTTAG TCACAATTAA TTCATGTTAA	4380
ATCATCAATA GTTTGGATT GGAGGGAGTA CTCATTAGGA AAAATAATTA AGCTAAATCA	4440
TTCTTATTT CACTGTACAT TATTAGATT AAGGGTGAAG TAGGGGAGGA ATCAATTATC	4500
TTATTTCTT AAATGGACAA GTATTTGAA ATAACAAATT TAAAGAAAAC ACCTCAAGTC	4560
AAATAGAGTA GGATGGATGG AGTAAATTCTT AACTCTCTA GATATTCTAA AAAATTAGTT	4620
GAACAGACAT TTAATAAAG ACCACAAGTT GATGAATTAA GCTTGTGTT CCAATATAAT	4680
TGGGATTAAC ATGAGATCTT GTGGCAGTAA TGTTTTGC TTGTTGCAA TTGTTCAATA	4740
AAAAGAAAAC ACTTGATGG GTCACTTAA TACAAGTTG GAAACCAATC ACGTTATGTG	4800
GTCATACTT TTGTTGAGTA ATGTAATAAT ACCAATAGTG GGGCCCCAC TCAAGTAAT	4860
CCATCTTCCA CTGATTTTTT TTATTTTTT TTGAAATGGA GTAGGTTATC TTGGCCGCTT	4920
AGCAATTACT ATTATCATGA GTAAATGAGC GAAATTATAA ATTTTTAAGA TAAATTATT	4980
ATTAATCTT TATAATTAA TGGTTATAAA AGTCTCTAA ACTAATACAA TAATATAAGC	5040
GCTGATACAT GAGTCYATG TGCGAGATAC ATTATCTGA TAGTTAAAAA TGAGGAAC	5100
GAAATTATA AAACAAATAT GAATAATGAT AATAAGATAA CTAAATGTG AAATTCTAT	5160
CATTCTCTT ACACATACCAC TAGTGAAATT TGTTCAGTA TCTTGTGAA GAAATCTTA	5220
TCCAAAAGTC AAAAATAAAA ACTCGTGGCC AAATTTCAA AAAAAAAGA AGGTTATCTT	5280
TTTGGCCAA AAAGCATAGC AATTTGGTA CGGAACGTAT TGAGATTTG TAGAGTATT	5340
TATAATTCAA ATTGCATAGA AAAGCTTAC CTACACAGT AAAACTTG AAATTCTAT	5400
TAACGTGAAT AAATTGGTA ACAGGACCAT TGTATCACAA GGGATGGTAC CACCTTTTT	5460
ATCAATACAA TCCAGATTCA GCTATTTGGG GAAATATCAC ATGGGGCCAT GCTGTATCCA	5520
AGGACTTGTG CCACTGGCTC TACTTGCCTT TTGGCCATGGT TCTGTATCAA TGGTATGATA	5580
TTAACCGGTGT CTGGACAGGG TCCGCTACCA TCTTACCCGA TGGTCAGATC ATGATGCTT	5640
ATACCGGTGA CACTGTATGAT TATGTGCAAG TGCAAAATCT TGGTACCCCC GCACATTAT	5700
CTGATCTCTT CCTCTAGAC TGGGTCAAGT TCAAGGCAC CCCGGTTCTG GTTCCCTCAC	5760
CCGGCATTGG TGTCAAGGAC TTAGAGACC CGACTACTGC TTGGACCGGA CCACAAAATG	5820
GCCAATGGCT GTAAACAAATC GGGTCTAAGA TTGGTAAAC GGGTGTGCA CTGTTTATG	5880
AAACTCCAA CTTCACAAAGC TTAAAGCTAT TGGATGGAGT GCTGCATGCG GTTCCGGTA	5940
CGGGTATGTG GGAGTGTGTG GACTTTTACCGTATCTAC TAAAAAAACA AACGGGTTGG	6000
ACACATCTAA TAACGGGCCG GGTGAAAGC ATGTGTTAAAGCAGAATTTA GATGACAATA	6060
AGCAAGATCA TTATGCTTATG GTGACGTATG ACTTGGGAAAGAACAAATGG ACACCCGATA	6120
ACCCGGAAATT GGATTTGGA ATTGGGTTGA GACTAGACTA TGGGAAATAT TATGCTCAA	6180
AGACTTTTA TGACCCGAAG AAAGAACGAA GAGTACTGTG GGGATGGATT GGGGAAACTG	6240

-67-

ACAGTGAATC TGCTGACCTG CAGAAGGGAT GGGCATCTGT ACAGGTATGG ACTTGGATGA	6300
ACACATTGTT TTGTTATTT ACTTTGCACC ATACACAGCG TCTAGTTGTA TCGTAATAAT	6360
CATGGTAGGG AAATTCTTA TTAGAGAAA GTTGTATAA TCAATGCATT TGTAGGTGAA	6420
GTAAATTCTG AATTGTATAT GAAACGTGTC TAATAGTGT TCGAAATAAC AGAGTATTCC	6480
AAGGACAGTG CTTTACGACA AGAACAGGG GACACATCTA CTTCAGTGGC CAGTGGAGA	6540
AATTGAAGC TTAAGAGTGG CTGATCCTAC TGTTAAGCAA GTCGATCTC AACCAAGGCTC	6600
AATTGAGCTA CTCCGTGTTG ACTCAGCTGC AGAGGTTTGT TCGGTTACTT TTGTTTAA	6660
TTACAAACAC CGCGCTTAATC TGCGAGTCCC AAACCTGTT AGCTATTGTG CAGTGGATA	6720
TAGAAGCCTC ATTGAAAGTG GACAAAGTGG CGCTTCAGGG AATAATTGAA GCAGATCATG	6780
TAGGTTTCAG TTGCTCTACT AGTGGAGGTG CTGCTAGCAG AGGCATTTG GGACCATTTG	6840
GTGTCATGT AATTGCTGAT CAAACGCTAT CTGAGCTAAC GCCAGTTAC TTTACATT	6900
CTAAAGGAGC TGATGGTCGT CGAGAGACTC ACTTCTGTGC TGATCAAAC AGGTTTGCTT	6960
TTCTATCTGG CACAATTAAAT TTGTCCTTGT AAAATGGAGA TGGATAAAAG TAGCGGGTTG	7020
TTGATCTGAT ATATGCAGAT CCTCTGAGGC TCCGGGAGTT GTAAACAAAG TTATGGTAG	7080
TTCACTGTTGAGC GTGAAAAAACA TTCAATGAGA TTATGGTAA GTGATAATGA	7140
TTCCCTTATT TTACCTTGAT TTTATTCAT TTCTTCACCTT CACAATAATT AAAGTACTTG	7200
GCAGTTGCAT TTGAGTAAAA GGTTTTTAT AAACGTGATT TTAGGTGGAT CACTCAATTG	7260
TGGAGAGCTT TGCTCAAGGA GGAAGAACAG TCATAACATC GCGAATTTAC CCAACAAAGG	7320
CAGTAATGG AGCAGCACGA CTCTTGTGTT TCAACAATGC CACAGGGGCT AGCGTTACTG	7380
CCTCCGTCAA GATTTGGTCA CTTGAGTCAG CTAATATTCA ATCCCTCCCT TTGCAAGACT	7440
TGTAATCTTC TTATTTCTGTT TTATTTTTC TTTCATTTT GAAGGTATT TCACTGACGT	7500
CCCATCAAGA AAGGAAAGAG GGAGATCAAT ATATGTAGT TATTCGCC TACCTTAGGA	7560
TTAGATGTCA TCTAGCAATG TCAAACTCTAG TAGACTATAC AATGTATGGG TTCCCTGGAAA	7620
CCGAGTAGAG CTTACCTGGA TTCTATGAA ACTAAGAAAG CTCAGCAAAT ATATGCACAA	7680
ATAATTTACA GAAACAACTT GGGATGTTG ACAAACTTGA TTATTTTTC TTTCATATAA	7740
CTAGTAATAA CGGCAAGCTC TCCGCAATCT CGTTGAGCAA AAGTATAAT GTTACGGAC	7800
CACCTAAATA TTTCATGTCAC ACAGAGATTGG AATTGGAGCT TTTATACAC AACATATACA	7860
ACAATGATTC ATCTTCTAAC TCATACAATT CTATACGTA GGTCGAAGTT AGGAGGGAGT	7920
GAGCAACTG GTAAAAAGTA TATGGTATAA GTAAAGATATT TTAAATGTA TTATGTATCA	7980
GTGACTCTCA ATCAAAGGC GGATAAATAC AATTGATACA ATATACAAA TAGTTATGCA	8040
CTAAATAATA AATAGAGGAT AAAATGTAAA AGAAATACAA AATATAATC TCTCGATCTC	8100
GCTCCCGTCT CTCCCTCTCTC GATCTCACTC ATCTCTCTTC TCTTAATATG TATTCTTTT	8160
AATACAAATT AGTTCTATT TGTATTTTT CTTCAAATT CACGAAAAAA AATATATATA	8220
AATATAATG CATAGCGAAC AAGAATATTA TTATGAATCA TAAATAATGA AACTGTAGTT	8280
ATGGAATACT TTAAAGGGTT AATGTTGTT GTTTTGAAA TTTCCTCT TGAGCCCTT	8340
AAAGTCAAAT CTTGAATCCA CTATGAATAT GATTCTTCTT TTATACATAT ACAATAATAA	8400
TGATACATT CTATTTACGA ATGATATAAT TCCCGTACAA ATAATTTAG AGTTACAAAAA	8460
GAAGATCAGC CCAGCCCCATC TAATTCAAGC CTCGTGGGCC AAGAAATTAA ATGAGCTAAG	8520
GAAGGTGGC CCTTTATTTG AAAGTGCCTA AATTGTCAA CTCAACCTAA TTTAGAAGG	8580

-68-

CCCACAAACT GGGGGGGTTA GCATTTTTT CTTTAAAGCTC TATAACCATCA 8640
 AGTAAATGAG ACTATTTTC AATCAAATAT GTAAACAATG GTGTTTTTC AATAACACTA 8700
 ACAAAAAATT TGATGTGATTA ACATGTACCT TGGATACACT ATGCCCAAGC TACATGTATA 8760
 TGTGATGATG CATTCCAAT ATGCAAGCGA GATAAGAGCG ACCAACAGATGG GTGGGAGGCG 8820
 AGGGCTTGGGA ATTGTTTAT ATATCCCTAGA TACATGCCAA TCCATTGAA TGAAGTCCTT 8880
 CTAGAATAAA TAGACGTATC GAAATGCACC AAAATCTAGT AGAGTTGTA ATGTTACAGC 8940
 ATAACGTGCA TCTAAGTAAT TAGCTAGCTC ATACACTAGT GAGATCCTT TAGTTACCGT 9000
 ATATAAAATAG TTTTGACCCA TGGGACGATC CTAACCTGTT CCCGATCAAG ACTCAAGGGC 9060
 TTATAAGTCC TAATGTTGAA TGGTCTTGTA AATCCCTATCA CAACCATACC CCAATACCGA 9120
 GTTGGGTTGG ACCGGCTCCA TGGGCTTAGC AAACCTTGAC ATATCTACAC ATAATGGAC 9180
 AAATGAAAAA AAAATACGA AATGAAATTA TTTTTAAAC AATAAGACA ATATTTTTT 9240
 AGAGAAAGTT ACAAAATTAT ATACAACTTA ATATTATTAT ATCCCTCTAA AATTCCCTATC 9300
 TTGAAATTAA ATACAAAAT TTCCCTTTTC CCTCTCTCTC TTTTTCTAC CGGATACATC 9360
 ACTCGACCTC TATGAAATAC ACCACAATT TGTGTTGTA TACTAATATG GTAGAAATAT 9420
 TATTACCGAT ACATAACCCC AATTATTCA AATATAATTAA TATTAGTGTACACAACTTA 9480
 TTTATGTTT GTTATATATA TAGAGCGAT GAGCAATGTA TCCACAAGTT TTGAAAATC 9540
 CAAATCATT TATTTAAAAA ACCTTTAAGA TAATGTTGAA TTAACGCCAA AAAACTATTG 9600
 AGGTTCTGT ATTCTGTATT GTATTCCCTT TAAGGAAAAA TATATAATAA CAAACTATTA 9660
 ATTCAAATTA AATGTTATAT ACACAATTG ATTTAACCTG TAGCAAATAA TTTTCATTG 9720
 CCTCTCTCCC TAGGTTCTC ACTCGCCACT CTCGCTTTA TACAAACACA AATGTATAAA 9780
 ATGTTGTTGT GTTTGTATAA AGCGAGAGAA AATGTATATA CAAATATGAA TACATATATT 9840
 TTCGCTCTAT ATACTTATAA TGATACAAAT ACAGATCTT TCCTATCCAG TTCTCTTTG 9900
 TCTTCTCAC TTATACAAA CACAAATTAT ACAATTACA ATGTATAATT ATTGTTGCAT 9960
 AAAGCGAGAG AGAGATTGCA TATACAAATA GTTATTTCG ATTCAATTAT ATATAATTC 10020
 AAATTTATG CAGATATGCA ACAAAATAA ATAAAATTG AGGGCTGTC AGCGATTAT 10080
 GCCAACGATT TATACAAATG ACCTACCACCC GAAATTATAC AAATCTGAAG CATTGCCAGC 10140
 GAGCTATACA ATCTGATGCT CCATAACAAA CATAAAATT ATCATGGAAC GTAATATAC 10200
 AAACTATGAC TATAACATTCA AATATAATT TTATGTTTG CCATATATGA AAATTGATCT 10260
 - AAGCCTTTCG AACTATCCGA TGTCAATAGT TTCAACCCAGA TAGCCATTAA TATCAAAGTT 10320
 CAGGCCAGA TCATTGGGAT AATTGGGCC TATATTGTGG ACCGTGACTC GAAAACACC 10380
 TAATGCTACA GGCTACACCA AATTGATTAA TGATTTCTCA TCTCTGAAA ACAAAATAAA 10440
 TTATATAATT TTATATTACA TAAATATTTT TTCCCGCTA AATTCAAAGT AGTCAAACAT 10500
 TCAAAATAT TTAAACTGAT AATCAGAGCT CAACTCACCT TTTCATTTAT ACTATTATTA 10560
 TATTTTTTA ATATTAGAGA CAAAAAGAA AAGCTCTCAT ATTAATAAT AAAATATATA 10620
 GAATTGACAG ACCATTGTA CCATTCTCT CATAGTTAA ATAGTATATA ATTGGGCTCG 10680
 ACTTTATATA AATTCTGTAT ATATTATTTA ATATCTCTT TTGCTTTCC TTTCTGCAT 10740
 TACTTTTTT TTCCATTAA ATAATAATAC AGGTTATGG GTATTATAAA ACGGATCC 10798

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4032 base pairs
- (B) TYPE: nucleic acid

-69-

(C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Lycopersicon esculentum(ix) FEATURE:
 (A) NAME/KEY: precursor_RNA
 (B) LOCATION: 889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCAAATT	AGTTTGACA	TCTTCTTCAC	ATTCAGCA	TTAAACCAA	TTAACACTGT	60
TTTATTATTA	TTATTATATT	AATTAAATT	TTCTGAGTTT	AATTTTATT	TTCTAACATT	120
ATTTTATA	CTTTCATTG	AAAAATTGCA	TTGTTTATAT	TCTTACTTCA	TAATGTACGT	180
ATATAACATT	CTTTGCAGAC	TTCATTTATG	AAATTACACT	ATAGAATAAT	AATTGATT	240
ATATGTACTT	CCTTCCTTTC	AAATTGATTA	AATTGTTAAG	GTGTTTCACA	CATTAAAAT	300
AAATTAAAGTC	ACATATTAAAG	CATACTTAA	AATTTTACA	AAATAAGAG	CTCTCTATAA	360
AGTTTGACTT	TAAGTCTCCA	AATTGTTAA	TACAGACCTG	AAAGAGTGT	GGAGCTAAC	420
AAACAAATAG	TTATAAAAAG	TAATTTTATT	CAATTTTATA	GAATTAAAAG	CTATATGTGC	480
ATACACCAAA	ATTTTACATC	CTTATCATA	GCAAAATTAA	TAGAAAATAA	AAATAAATT	540
GTAACATG	TTTTTTTTT	CAACACTGT	AAAACCGAA	AAAATTGCT	AATGTGTAG	600
AAAACATGTG	TAATATAAA	CAATATAAA	AGAGTCCACG	TGCATCGCAT	GAGTACCTAT	660
ATTAATTAA	GCTGAAAAT	AAAATTAAAT	ATTTTTTAT	TCAAACACT	ACCAATTATT	720
ATAAAACAT	TTAACTTAAT	TGGATGCACC	AACTTTGACA	GGTGTAAATT	CACTTCATA	780
TTCAACCAAA	AAAAAAAAGA	AGGTTAAAAC	GCAAAGCAAC	TTAATTCTT	TGTTATAAAT	840
TGGAGGAGCC	AAAGATAGTG	AGATTCACAA	AACTTTATAT	CTCTAAGAAT	GGAAATTCAA	900
AAGGTATCAT	AGTTTCTAAT	ATTTTTTTA	ATTATATATG	TCTATCTAA	GTTTCATTCA	960
TATACTCATG	ATTAATTAT	TGATCATTT	AAACAATGAA	ACATATCTT	GATTAAATT	1020
TATTTATTAA	TTTTTATAAC	ATAGGAGTTT	GATTTAACGA	TAGTTCCAAC	AGAAGGTGAA	1080
ATTGATGCAC	CATCATCGCC	AGGAGAAAT	TTATGTCCTA	GTGTGATGGA	ATCTGATATT	1140
AAAATGAAA	CGCTTTTCA	AGAACTCGAC	ATGATTITGA	CTCAATATT	AGAGACATTG	1200
TCCGAGCGAA	AAAAGTATCA	TATAGTAAG	GATATACATA	TGTATAGTCT	TTCCATACAA	1260
ACATAGTTAC	TTTTTACTCA	ACGAAATTAT	ACAAGCATT	TAGTGTGCGA	GGTAATTAA	1320
TCTCAATTAA	ATTTAAATAA	ATACATTTC	ATTTTTTT	ACGTGTGAA	AAACATAAA	1380
AGTATTATA	AGAAAATTAA	ATCAAAGTT	ATTCAATT	AAATCATCCC	TAACTTATT	1440
TTTACATATC	TTTTAAGTAT	TTTGATTTG	GCCAAATAAT	ATTTACGAT	TTTATTCTATA	1500
ATTATATCTT	TGGTATTAA	ATTCACAGT	TATCCATTAA	ACATGTGTT	CGAACATCAT	1560
GCCACTTTAG	CCCCACTTTT	GCAATTTCAT	TTGAAACATT	GTGGGAGATCC	CTTTACTCG	1620
CACCCCTACAG	ATTCATTC	AAAAGATT	GAAGTGGCTG	TTTTAGATTG	GTGACCAA	1680
CTCTGGGAAA	TAGAGAAAAGA	TGAATATTGG	GGNTACATTA	CTAGTGGTGG	CACTNAGGGC	1740
AATCTCCATG	GCCTTTGGT	TGGGCAGGTA	TCATTTCAA	GAAAGGGGGT	GGGGGGAGAG	1800
GTGGTAGTTT	TGAAATCATA	TGAAAATCA	AAAATTAA	TGGCGTAATC	AGCCATTGTC	1860
ATGGTCAAA	TCATTACCGAG	CAAGACGTCT	TACTTACTT	TTGTTGTACC	ATAGGTACAC	1920

-70-

AATCAATGAC AAATTGTAT TGGCACACAA TAATGACCAC AATCCCTCTA TGCAAGAGCT	1980
ATTTCTTCTT TTTCCCTT GCGGTAGTTC ACAATAAAC A TACCATAGTG ACCGATAAAC	2040
ATACAGTAGC ATTAGCCATT TTGCCAAT AAAATTATT TTCTCTCAA CCTCCCGTAG	2100
AGGTGAGTT TGACATATAT TATTTTCT CAAACCTCT ATAGAGGTGA GTTGAGACAT	2160
ATATTCAATC CATAATGATT TTATCATATC TTGACCCATT CTCTTATAGA ATGGTCGAGC	2220
ATTCAATAA CTCATCACAA GTCACATTCT CTTCAAGGAA TTCATAAAATT TGTATTATAA	2280
GTACATITGC ATGGTTCTAA AATTCAATT ATTTCATGA CACACCTAA CATCACTTTG	2340
AAAGATCAAG TGTACCATCA CTTTATCTTC TTGTCTCATG ATAGAGGATT TATAAAGTTG	2400
TCAAATTGGG TCGACAACAT TCAGAAGTCC AATGACCTT CATAACCTTT TATAATAAAA	2460
ATTCTCTCA CATTITGAAG GACTATTGG AGAACCCATA GTGTTCTTCC TTTTATAATT	2520
ATCACAATGA TGACTTATT AATTCGTC CTTCACGCC TTATTCATAT CTTAATTATT	2580
TTGTCACTT TCAGACGAAT TATTTGTGC TACTACATTC ATATAATTGA ATGGAGCAAG	2640
TCAACAGATG GATTCAAG TTATCACATG TTGCTCCAT ATTCTTTCA AGGAATGGAG	2700
CAAATTAAAT ATGATGAATT TCAATACATT TCATAAAAA TATATTATT TGCCTCAGTC	2760
ATCATCTTAT CATCAATTG GTGCATGGAG ACTCAAACTC AATGTCTTAT CCATACAAGG	2820
CACATTAGGC CATAATTCTA TGGGACTTGA ACCCAATACC TTATCATTAT GGTCATCAA	2880
AACTCGAATT GTGCTTAC CCTCTGGTG CGATAGAACT TGAATCTACC GTCTTACCT	2940
CAAATTTTC TCATAATGAA TGACATAAT GAGTCTTTT TAAACAAATT TGATAACATA	3000
TTTGAGTTT TTTCTTATGG TAAATGATG CAAGTCTTC ATCACTTCA TAAAGCATT	3060
GAACAATATT ATATATTGTG GCAGAAGAGA GCTACTTCTT AATGGATATT ATATGCATCA	3120
AAAGATTCAAC ATTACTCGAT TTTCAGCA GCAAGAATGT ATCGAATGGA GCTACAAACT	3180
ATCAACACTT TAGTTAATGG GGAATTGAT TATGAAGATT TACAATCAA GTTACTTGTG	3240
AAACAAGAAC AACCAGCTAT CATCAATATC AATATTGGTA AAAATACATA CATAATATT	3300
CTTACATCTT ATAACATCAC TTTGGTAA TTGATATATA TGTGTTATA GGACACACCT	3360
TCAAAGGAGC TATTGATGAC CTCGATTCG TCATACAAC ACTTGAATAT TGTGGTTATT	3420
CAAATGACAA TTATTATATC CATTGGATG CAGCATTATG TGGGCTAATT CTCCCATTA	3480
TCAAACATGT AAGCTTATT TTATTCATT TTCCCTCAAC GCTCGATCGA AGTTACAATG	3540
ACATAGTTTC TTCTATGGT ATTGACAAT AGGCAAAAAA AATTACCTTC AAGAACCAA	3600
TTGGAAGTAT TCAATTTCA GGGCACAAAT TCTTGGGATG TCCAATGCT TGTGGCGTTC	3660
AGATAACAAG GAGAAGTTAC GTTAGCACCC TCTCAAAAT TGAGTATATT AATCCCGCAG	3720
ATGCTACAAT TTCTGGTAGT CGAAATGGAT TTACACCAAT ATTCTTATGG TACTGTTAA	3780
GCAAGAAAAG ACATGCTAGA TTGCAACAAG ATTCCATAAC ATGCAATTGA AATGCTCGGT	3840
ATTTGAAAGA TCGACTTCTT GAAGCAGGAA TTAGTGTAT GCTGAATGAT TTTAGTATTA	3900
CTGTTGTTT TGAACGACCT TGTGACCATA AATTCAATTG TGTTGGAAC TTGTGTTGCT	3960
TAAGAGGCAT GCCACATGTT GTAATTATGC CAGGTATTAC AAGAGAAACT ATAGATAGTT	4020
TCTTCAAAAGA TC	4032

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10965 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

-71-

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon pimpenellifolium*

(ix) FEATURE:

(A) NAME/KEY: precursor RNA

(B) LOCATION: 3686..7612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCTCGATA AGTTATGCT TGTGGAATC GATATCAAAT AACCGTCGAC GGTATCTTG	60
ATATGAGGTA GCGCTCAATG ATATAATG TGATGAGGAT CTTGAATTCA AATCTGTAT	120
ATAGTGTGAA CAGATAATG GTGGCCAAG TAAATGCAC AATTCAAGTA TATTTGTTT	180
CACTTAGAAA AGTGACATTG TGGACTGGTA GTCCATAAT CAAGGTATAA TGTCAGTGGG	240
GTACAATAA ATTATTATGT GATAGTATAA CCGTAAGATA TCAAATACGG TTGTCCTT	300
GGGGCATAAA AGTTTATCGC AAAATCCCTG ACATTATTGG AGATGTTTC TCCTTGGTG	360
GATGCAATGA GGTTTGTGTT GATCTGGCA CATATGAAAA ACTGAAATGC ATGAAATGAA	420
AAATTGTAAT GAAGGTTATA TGAAATCCT TGAAACAATC CAGGTGTCTG AAGCATATAA	480
AGGTTGAAAG AAACCTTACCA ATAAAGCTT CAAGAATCCT TATATGGATT GAAATAGTC	540
AGGAAGAAAA AGGGTACAAA AGAATGACCC TAATTGCTT TGATTTTTA TGAAAAGTC	600
TTGGTAAGAC AAAATTTGT CTTGACCTAC AGATTGTTAA TTGACAAAT AAAATATTG	660
TCTAACAGAC AACAGTGCAC ATACACTGAA AAATTTGAT GCAATTTAT GTGGATATAT	720
CGCATTCAATT GAGTACCCCA ATGATTATGA GATCACTTGA CATAAATGAT GATTCACTT	780
GATCTCAAAA AGGGATAAG AGTTTCTGG TGATGAAACT CTATCTGGT GCAATGAGGG	840
CACTAGTGCA TCTTACTAAC ATATTTGAC TAGATATTG TTGACAGTA AATTACTGG	900
CAAGATTCAAG TTTCTCCCCA ATAAAAGGAC ATTGAAATGG TGTTGAGCAC ATGAAATGAAT	960
ATCCTCAAAAG GACCATACTT ATGGGTTAT TCTATCCCAGA GGAATCCAAG ACAAAATTGA	1020
TTGATTACCC AGATGCAGAA TATTTATCTG ATCCGCATAA AGCTCTATCT CAAGCACGCT	1080
ATGTTGTTGC ATGTTGGAGGC ACAATAATAT CCTGGGATC AATGAAGCAA ATGTTGCTCT	1140
GCAGAAATAA AAGTCCTCCA TGAGCAAGT CAAAAGTGGG TCTGGTTGAG ATAATGACA	1200
CACCATATTC AAGAAATG TGTTTTTCTT TAAAAAAAG ATATACCAA CCACAATGTA	1260
CAAAGATTGG AGACATCATC ACAAGAAATC AAGTGATGTT TTAATCAGGG GGAGTACAAT	1320
ACCGCGTTGCA CTCTTTTCTC CTTGATCGAG GTTTTTTCC CACTGGATT TCTGACAAG	1380
GTTTTTAATG AGGCAACAAA TGGTGGTAT CAAAAGATAT GTGTACTCTT TTCTCTCAC	1440
TAGAATTCTT TCCACAGGG TTTTCCTAG TAAGGTTTA ACGGAGGCACA TTATCTATGG	1500
ACATCCAAGG GGGGGTGTAA TAAATACATT GAATTAAGTG GATAGTCCAT AAGGTTGGCA	1560
CATGAACAC CATTCAATT CACTAGTGA CATGAACCTT TTGATAAG AATGTATCTA	1620
TTTATTATGA TACTTAATAT GGTAATCTT GGAGTGATTT CTCACTCTAT AAATAGAGTT	1680
GTTCATTCACT TATTGTAATA TATACATATG AGACTTGAAAT ACACTGAAAT AGGAAGAAAG	1740
TCTTATCTTC CACTCTTACTT CTCTTGCTT CTCTCTTAT GATTATATTC TTATGAGCTT	1800
GATTTATAA CACGAATCTC ATTATACGA AAGTTTACT ATTATATTTT AATTAAGA	1860
GGATTTAAAC TTTTTAAATT TCTGCTTTA TAGATGAGAA CTGTCCTTT TGTTGAATCC	1920
AACTAAACAT TCAATGAAGA CAAATCAACC TGAAATCCC TTCAAGTAG GATTTATTG	1980

-72-

AATCTCATTA TACGAAAAGT TTACTATTT ATATTAATT ATAGAGGAT TAAACTTT	2040
TAATTTCTG TCTTATAGA TGAGAACCTG TCTTTTGTG GAATCCACT AAACATTCAA	2100
TGAAGACAA TCAACCTGTA AATCCCTTC AAGTAGGATT TATTCGAATC TCATTATACG	2160
AAAAGTTTA CTATTTATAT TAAATTATAA GAGAATTAA ACTTTTAA TTTCTGTCTT	2220
TATAGATGAG AACCTGTCTT TTGTYGAAT CCAACTAAC ATTCAATGAA TACAATCAA	2280
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-73-

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-74-

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-75-

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATTCTAGAA GATAGAGGAA TG

-76-

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGAAGCTTAA TCAACCTGTA AATCCC

26

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCATGCTC CGTCCTGTAG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTGCATGCCT GCAGTTGTTT GCCTCCCTGC TG

32

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AACTGCAGAA TGGAGCAGCA CGACTC

26

-77-

THAT WHICH IS CLAIMED IS:

1. Isolated substantially pure DNA, comprising a sequence of nucleotides that encodes a tomato vacuolar invertase.
- 5 2. Isolated substantially pure DNA, comprising a sequence of nucleotides that hybridizes to the DNA of claim 1 and that encodes invertase.
3. The DNA of claim 1, wherein said tomato vacuolar invertase is *Lycopersicon esculentum* or *Lycopersicon pimpenellifolium* invertase.
- 10 4. The DNA of claim 3, wherein the DNA that encodes invertase is genomic DNA.
5. The DNA of claim 3, wherein the DNA that encodes invertase is cDNA.
- 15 6. A substantially pure DNA fragment encoding a tomato fruit invertase, comprising the amino acid sequence set forth as residues 1-636 in Sequence ID No. 1.
7. The DNA fragment of claim 6, wherein the DNA encoding the tomato fruit invertase has substantially the same nucleotide sequence as set forth in Sequence ID No. 1.
- 20 25 8. The DNA fragment of claim 5, wherein the DNA encoding invertase has substantially the same nucleotide sequence as the portion of nucleotides 1-2199 set forth in Sequence ID No. 1 that encodes invertase.
9. Isolated DNA that hybridizes to the DNA of Sequence ID. No. 1 and that encodes invertase.
10. Isolated DNA that hybridizes to the DNA of Sequence ID. No. 2 and that encodes invertase.
- 30 11. Isolated DNA that hybridizes to the DNA of Sequence ID. No. 4 and that encodes invertase.
12. The DNA of claim 3 that does not include nucleotides of the sequence:

-78-

- 5'-AAACAACTTG GGAATGTTGA C-3',
which occur at residues 2164-2184 in Sequence ID No. 1.
13. A DNA construct, comprising the DNA of claim 1
that encodes invertase operatively linked to a promoter
5 which effects expression of heterologous genes in plants.
14. A DNA construct, comprising the DNA of claim 1
that encodes invertase operatively linked to a
developmentally regulated promoter, wherein said DNA
encoding invertase includes sequences that encode a
10 vacuolar targeting sequence.
15. The DNA construct of claim 14, wherein said
promoter region is the HDC promoter region.
16. The DNA construct of claim 14, wherein the
promoter region includes a sufficient portion of the
15 sequence of nucleotides set forth in residues about 1-889
of sequence ID No. 3 to effect developmentally regulated
expression of the DNA encoding invertase.
17. The DNA construct of claim 13, wherein the
promoter region is the promoter region from the
20 *Lycopersicon pimpinellifolium* or *Lycopersicon esculentum*
gene that encodes tomato fruit vacuolar invertase.
18. The DNA construct of claim 13, wherein said
promoter is constitutively expressed and the DNA that
encodes invertase includes sequences of nucleotides that
25 encode a vacuolar targeting sequence.
19. The DNA construct of claim 18, wherein the
promoter is the cauliflower mosaic virus 35S promoter.
20. A DNA construct, comprising DNA encoding all or
a portion of antisense invertase RNA operatively linked
30 to a promoter, wherein said portion is sufficient to
produce mRNA which is effective for inhibiting
translation of mRNA that encodes the invertase and said
promoter is developmentally regulated or is a
constitutive promoter and effects transcription of
35 heterologous genes in plants.

-79-

21. A DNA construct, comprising DNA encoding a portion of invertase mRNA operatively linked to a promoter, wherein said portion encodes a truncated protein that is effective, upon introduction into a host 5 cell, to cosuppress expression of endogenous invertase.

22. A method for increasing the soluble solids content of tomato fruit, comprising introducing the DNA construct of claim 13 into a plant cell to produce a transgenic plant that produces said fruit, whereby the 10 soluble solids content of the fruit, at harvest, is greater than that in tomato fruit produced by a wild type plant of the same species.

23. The method of claim 22, wherein said invertase is a tomato fruit invertase.

15 24. The method of claim 22, wherein the onset of expression of said invertase commences at an earlier stage of ripening of the tomato fruit than occurs when said plant does not express said invertase, and said expression continues throughout the ripening of the 20 tomato fruit.

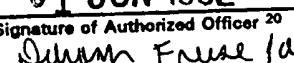
25 25. A method for altering the solids content of tomato fruit produced by a tomato plant, comprising introducing DNA encoding antisense tomato fruit invertase mRNA or DNA encoding a truncated form of said invertase into tomato plant cells to produce a transgenic tomato plant, whereby the tomato plant expresses sufficient levels of antisense tomato fruit invertase mRNA or truncated invertase to reduce the total amount of tomato fruit invertase expressed in said plant such that the 30 total amount of tomato fruit invertase in said transgenic plant during fruit ripening, is less than the amount of tomato fruit invertase produced by a tomato plant, which does not express antisense invertase mRNA or truncated invertase and which is a member of the same species as 35 the transgenic plant.

-80-

26. A transgenic plant, comprising the DNA of claim 1.
27. The transgenic plant of claim 26, wherein said plant is a tomato plant.
- 5 28. A plant protoplast, comprising the DNA of claim 1.
29. The plant protoplast of claim 28, wherein said protoplast is a tomato plant protoplast.
- 10 30. A tomato fruit produced by a transgenic tomato plant of claim 27.
31. The tomato fruit of claim 30, wherein said transgenic tomato plant is a species of *Lycopersicon esculentum* or *Lycopersicon pimpinellifolium*.
- 15 32. A seed produced by the transgenic plant of claim 27, wherein said seed contains DNA that encodes heterologous invertase.
- 20 33. A method for the recombinant production of tomato fruit invertase, comprising expressing, in a recombinant host, DNA encoding a tomato fruit invertase having substantially the same amino acid sequence as the amino acid sequence set forth in Sequence ID No. 1.
34. An invertase promoter region encoded by the DNA of claim 4.
- 25 35. The promoter region of claim 34, included in nucleotides 1-3519 of Sequence ID No. 2.
36. The promoter region of claim 34, included in nucleotides 2772-3519 of Sequence ID No. 2.
37. The promoter region of claim 34, included in nucleotides 2440-3519 of Sequence ID No. 2.
- 30 38. The promoter region of claim 34, included in nucleotides 1-3679 of Sequence ID No. 4.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US92/01385

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) ³					
<p>According to International Patent Classification (IPC) or to both National Classification and IPC</p> <p>IPC (5): C12P 21/00; C12N 5/10, 15/09; A01H 5/00; C07H 15/12 US CL : 435/69.1, 172.3, 240.4; 536/27; 800/205</p>					
II. FIELDS SEARCHED					
Minimum Documentation Searched ⁴ <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left; padding: 2px;">Classification System</th> <th style="text-align: center; padding: 2px;">Classification Symbols</th> </tr> </thead> <tbody> <tr> <td style="padding: 2px;">U.S.</td> <td style="text-align: center; padding: 2px;">435/69.1, 172.3, 240.4; 536/27; 800/205; 935/35, 60, 64</td> </tr> </tbody> </table>		Classification System	Classification Symbols	U.S.	435/69.1, 172.3, 240.4; 536/27; 800/205; 935/35, 60, 64
Classification System	Classification Symbols				
U.S.	435/69.1, 172.3, 240.4; 536/27; 800/205; 935/35, 60, 64				
Documentation Searched other than Minimum Documentation to the extent that such Documents are included in the Fields Searched ⁵					
<p>APS, DIALOG search terms: invertase or fructosidase, tomato or lycopersicon, vacuol?, cosuppress?, histidine decarboxylase</p>					
III. DOCUMENTS CONSIDERED TO BE RELEVANT¹⁴					
Category ¹⁵	Citation of Document, ¹⁶ with indication, where appropriate, of the relevant passages ¹⁷	Relevant to Claim No. ¹⁸			
X/Y	<p>The Plant Cell, Volume 2, issued November 1990, Sturm et al, "cDNA cloning of carrot extracellular B-fructosidase and its expression in response to wounding and bacterial infection", pages 1107-1119, see page 1109.</p>	2,9-11/20			
Y	<p>US, A, 4,801,540 (Hiatt et al) 31 January 1989, see entire document.</p>	1-14,16-20,22-25,33			
Y	<p>The EMBO Journal, Volume 9, No. 10, issued October 1990, Schaewen et al, "Expression of a yeast-derived invertase in the cell wall of tobacco and <u>Arabidopsis</u> plants leads to accumulation of carbohydrate and inhibition of photosynthesis and strongly influences growth and phenotype of transgenic tobacco plants", pages 3033-3044, see entire document.</p>	18-19			
Y	<p>Plant Cell Physiology, Volume 31, No. 5, issued May 1990, Endo et al, "Size and levels of mRNA for acid invertase in ripe tomato fruit", pages 655-659, see entire document.</p>	1-14,16-19,22-38			
Y	<p>US, A, 4,394,443 (Weissman et al) 19 July 1983, see entire document.</p>	1-14,16-19,22-38			
<small>* Special categories of cited documents:¹⁵</small> <small>"A" document defining the general state of the art which is not considered to be of particular relevance</small> <small>"E" earlier document but published on or after the international filing date</small> <small>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</small> <small>"O" document referring to an oral disclosure, use, exhibition or other means</small> <small>"P" document published prior to the international filing date but later than the priority date claimed</small>					
<small>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</small> <small>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</small> <small>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</small> <small>"&" document member of the same patent family</small>					
IV. CERTIFICATION					
Date of the Actual Completion of the International Search ² 13 MAY 1992	Date of Mailing of this International Search Report ² 01 JUN 1992				
International Searching Authority ¹ ISA/US	Signature of Authorized Officer ²⁰  P. RHODES				

FURTHER INFORMATION CONTINUED FROM THE SECOND SHEET		
Y	US, A, 4,446,235 (Seeburg) 01 May 1984, see entire document.	1-14,16-19,22-38
Y	US, A, 4,943,674 (Houck et al) 24 July 1990, see entire document.	1-14,16-19,22-38
Y	Phytochemistry, Volume 14, issued 1975, Manning et al, "Distribution of acid invertase in the tomato plant", pages 1965-1969, see entire document.	22-25
V. <input type="checkbox"/> OBSERVATIONS WHERE CERTAIN CLAIMS WERE FOUND UNSEARCHABLE¹		
This international search report has not been established in respect of certain claims under Article 17(2) (a) for the following reasons:		
1. <input type="checkbox"/> Claim numbers ___, because they relate to subject matter (1) not required to be searched by this Authority, namely:		
2. <input type="checkbox"/> Claim numbers ___, because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out (1), specifically:		
3. <input type="checkbox"/> Claim numbers ___, because they are dependent claims not drafted in accordance with the second and third sentences of PCT Rule 6.4(a).		
VI. <input checked="" type="checkbox"/> OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING²		
This International Searching Authority found multiple inventions in this international application as follows: Please See Attached Sheet.		
1. <input checked="" type="checkbox"/> As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims of the international application. (Telephone Practice)		
2. <input type="checkbox"/> As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims of the international application for which fees were paid, specifically claims:		
3. <input type="checkbox"/> No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claim numbers:		
4. <input type="checkbox"/> As all searchable claims could be searched without effort justifying an additional fee, the International Search Authority did not invite payment of any additional fee.		
Remark on protest		
<input type="checkbox"/> The additional search fees were accompanied by applicant's protest. <input type="checkbox"/> No protest accompanied the payment of additional search fees.		

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category*	Citation of Document, ¹⁸ with indication, where appropriate, of the relevant passages ¹⁷	Relevant to Claim No. ¹⁸
Y	Biochimie, Volume 70, issued 1988, Lauriere et al, "Characterization of B-fructosidase, an extracellular glycoprotein of carrot cells", pages 1483-1491, see page 1484, first full paragraph and page 1490, second and fourth full paragraphs.	1-14, 16-19, 26-32
A	Trends in Biotechnology, Volume 8, issued December 1990, Jorgensen, "Altered gene expression in plants due to <u>trans</u> interactions between homologous genes", pages 340-344, see entire document.	21

FURTHER INFORMATION CONTINUED FROM PREVIOUS SHEETS

VI. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

- I. Claims 1-13, 22-24, 26-32, drawn to a first product and process of use, classified in Class 536 and 800, subclass 27 and 805, respectively, for example. species (a) claims 14-16
(b) claim 17
(c) claims 18-19
- II. Claim 20, drawn to a second product, classified in Class 536, subclass 27, for example.
- III. Claim 21, drawn to a third product, classified in Class 536, subclass 27, for example.
- IV. Claim 25, drawn to a method of using the second product, classified in Class 435, subclass 172.3, for example.
- V. Claim 33, drawn to a second method of using the first product, classified in Class 435, subclass 69.1, for example.
- VI. Claims 34-38, drawn to a fourth product, classified in Class 536, subclass 27, for example.

I. Claims 1-13, 22-24, 26-32, drawn to first product consisting of a coding region and constructs and plants containing same and a first method of using same, classified in Classes 435, 536, and 800, subclasses 172.3 and 240.4, 27, and 205, respectively, for example.

The following are independent and distinct species pertinent to the invention of Group I where a) is the first species and will be searched with claims 1-13, 22-24, and 26-32 in the event that no other fees are paid. Note that a search of any other additional species within Group I requires payment of additional fees.

- a). HDC promoter (claims 14-16)
- b). invertase promoter (claim 17)
- c). constitutive promoter (claims 18-19).

II. Claim 20, drawn to second product consisting of antisense DNA, classified in Class 536, subclass 27, for example.

III. Claim 21, drawn to third product consisting of coding region for truncated protein, classified in Class 536, subclass 27, for example.

IV. Claim 25, drawn to method of using second product, classified in Class 435, subclass 172.3, for example.

V. Claim 33, drawn to second method of using first product, classified in Class 435, subclass 69.1, for example.

VI. Claims 34-38, drawn to fourth product consisting of a promoter, classified in Class 536, subclass 27, for example.

The inventions are distinct, each from the other because of the following reasons:

The products of Groups I-III and VI are unrelated and mutually exclusive inventions and are capable of separate manufacture and use and have different properties as claimed and thus are distinct inventions. The methods of Groups I and IV-V are also unrelated and mutually exclusive inventions involving different method steps and results as well as different products of use and products made and are distinct. The species a)-c) of Group I are unrelated and mutually exclusive and capable of separate manufacture and use and have different properties as claimed and confer different properties on the DNA constructs incorporating the species and are distinct.

Inventions of Group II and Group IV are related as product and process of use; the inventions of Group I and Group V are also related as product and process of use. The inventions can be shown to be distinct if either or both of the following can be shown: (1) the process for using the product as claimed can be practiced with another materially different product or (2) the product as claimed can be used in a materially different process of using that product. In the instant case each of the products of Groups I and II can be used in a materially different process such as molecular probes in hybridization reactions or as primers for PCR and DNA sequencing reactions, for example.

These inventions are distinct for the reasons given above and have acquired a

FURTHER INFORMATION CONTINUED FROM PREVIOUS SHEETS

separate status in the art as shown by their different classification, recognized divergent subject matter, and separate search requirements.

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